

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 19:18:54 ; Search time 3648 Seconds
(without alignments)

12292.993 Million cell updates/sec

Title: US-10-798-896-1

Perfect score: 5423

Sequence: 1 ccaccgggtggcgccgctc.....ctatagggaattggagct 5423

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5423	100.0	5423	9	US-10-798-896-1
2	2237	41.3	2237	9	US-10-798-896-5
3	2218	40.9	3599	3	US-09-861-101-3
4	2218	40.9	3803	9	US-10-798-896-2
5	2215.8	40.9	3600	3	US-09-861-101-2
6	2211.6	40.8	3558	7	US-10-281-067B-26
7	2211.6	40.8	3558	8	US-10-764-818A-26
8	2160	39.8	2192	5	US-10-021-403A-10
9	2160	39.8	3534	5	US-10-021-403A-9
10	2160	39.8	3534	7	US-10-395-709-11
11	2160	39.8	3534	7	US-10-395-709-12
12	2160	39.8	3534	7	US-10-395-709-13
13	2160	39.8	3534	7	US-10-395-709-14
14	2160	39.8	3534	7	US-10-395-709-15
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24	2160	39.8	3534	7	US-10-315-907A-15	Sequence 15, Appl
25	2160	39.8	3534	7	US-10-619-939-1	Sequence 1, Appl
26	2160	39.8	3534	7	US-10-281-067B-11	Sequence 11, Appl
27	2160	39.8	3534	7	US-10-281-067B-12	Sequence 12, Appl
28	2160	39.8	3534	7	US-10-281-067B-13	Sequence 13, Appl
29	2160	39.8	3534	7	US-10-281-067B-14	Sequence 14, Appl
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36	2160	39.8	3534	8	US-10-166-356-8	Sequence 8, Appl
37	2160	39.8	3534	8	US-10-166-356-9	Sequence 9, Appl
38	2160	39.8	3534	8	US-10-764-818A-11	Sequence 11, Appl
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41	2160	39.8	3534	8	US-10-764-818A-14	Sequence 14, Appl
42	2160	39.8	3534	8	US-10-764-818A-15	Sequence 15, Appl
43	2160	39.8	3534	8	US-10-764-818A-29	Sequence 29, Appl
44	2160	39.8	3534	8	US-10-827-918-11	Sequence 11, Appl
45	2160	39.8	3534	8	US-10-827-918-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-798-896-1
; Sequence 1, Application US/10798896
; Publication No. US20050238624A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS, Inc.
; TITLE OF INVENTION: Insulin-Like Growth Factor ("IGF-I") Plasmid Mediated Supplementa
; TITLE OF INVENTION: Therapeutic Applications
; FILE REFERENCE: 108328.00172 - AVSI-0034
; CURRENT APPLICATION NUMBER: US/10/798,896
; CURRENT FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 5423
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid sequence for the pAV2001 plasmid.
US-10-798-896-1

Query Match		100.0%;	Score 5423;	DB 9;	Length 5423;
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Qy	61	GGGTGAGGAATGTTGGGGAGTTATTTTAGAGCGGTGAGGAAGTGGCGAGGACGAGGT	120		
Db	61	GGGTGAGGAATGTTGGGGAGTTATTTTAGAGCGGTGAGGAAGTGGCGAGGACGAGGT	120		
Qy	121	GTGGCGCTCTAAAAATAAATCTCCGGAGTTATTTTAGAGCGGAGGAATGGTGGACACC	180		
Db	121	GTGGCGCTCTAAAAATAAATCTCCGGAGTTATTTTAGAGCGGAGGAATGGTGGACACC	180		
Qy	181	CAATATGGCGAGGTTCTCTCAGCGGTGCGCATATTTGGGTGTCGCGCCCTCGCGCGGGC	240		
Db	181	CAATATGGCGAGCGTTCTCTCAGCGGTGCGCATATTTGGGTGTCGCGCCCTCGCGCGGGC	240		
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Db	241	CGCATTTCTTGGGGCGGGCGGTGCTCCCGCCCGCTCCGATAAAAGGCTCCGGGGCGGGC	300		
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Db 361 AAGGCCCAACTCCCGGAAACACTCAGGGTCTGTGGAGACAGCTCACTAGCTGCCAATGGGA 420
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4741	Db		ACTTTCTCGGCAGGACGAAGTGCAGATGACAGAGAGATCTGTCCCGCGCATCTCGCCCAAT	4800
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5161	Db		TTTACTTTGAGGGCTTCCCAAACCTTACAGAGGGCGCCCGAGTGGCAATTCGGTTTCG	5220
5221	Qy		CTTCTCTCCATAAACCGCCGCTAGCAACCTGTTGGGAAGGGCGATCGGTGGCGGC	5280
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5401	Db		TC ACTATAGGGCGAATTTGGAGCT	5423

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RESULT 2
US-10-798-896-5
; Sequence 5, Application US/10798896
; Publication No. US20050238624A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS, Inc.
; TITLE OF INVENTION: Insulin-Like Growth Factor ("IGF-I") Plasmid Mediated Supplementation of Bone
; TITLE OF INVENTION: Therapeutic Applications
; FILE REFERENCE: 108328.00172 - AVSI-0034
; CURRENT APPLICATION NUMBER: US/10798,896
; CURRENT FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2237
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for the skeletal alpha actin 3' end.
US-10-798-896-5

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2014 TTGCTTTATGATGATGCTGAAGAGTGCCTTTCTTCTCACTGTAATGATTTTGGCCCTCA 2073
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2314 GGAGAGTATTTCCCAACCTCGCTGCTGACCCCTGATCTGGGGTTTCTCTGAGCTTA 2373
1381 GGAGAGCTATTTCCCAACCTCGCTGCTGACCCCTGATCTGGGGTTTCTCTGAGCTTA 1440
2374 AGCGGTGCCAAGTCTTAAGTGAATGTAGAACTAGTAAGCTGGAAAAGACACAGATCA 2433
1441 AGCGGTGCCAAGTCTTAAGTGAATGTAGAACTAGTAAGCTGGAAAAGACACAGATCA 1500
2434 TTAAGTCCAACTGTACGCCCATCCCAACCGCCCACTGTCACTCAGTGCACATCCAC 2493
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2494 GCATTTCTTGAAATCTCCAGGACAGTGAATCCACCGCTCAGCAGTGTGCTTTCAGAGC 2553
1561 GCATTTCTTGAAATCTCCAGGACAGTGAATCCACCGCTCAGCAGTGTGCTTTCAGAGC 1620
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1621 AGCAGGCTGACAGTCTCAGTGCAGTGTGATCTCCTGCTGAAGAGCTTAAACAGTGCAGTTT 1680
2614 AACACGGACTGATTTTGTGATGCTGTGATGATCAGTACGTGAGATGTCTCACTAAACT 2673
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1741 TTTTGAGATTAATTTTCAGATGGAACACATTTCTTAAACCTGAAACAGCCTTTGATTTG 1800
2734 GGCTTGGCATTTTCAGAAATTTGAGAAAGATTTTGGACACAGATGAATGGAATTTTC 2793
1801 GGCTTGGCATTTTCAGAAATTTGAGAAAGATTTTGGACACAGATGAATGGAATTTTC 1860
2794 CACCAACAGAAAATTAACACTTACACAGTGTGAGTCTGCTGCTTCTGATATTTCTT 2853
1861 CACCAACAGAAAATTAACACTTACACAGTGTGAGTCTGCTGCTTCTGATATTTCTT 1920
2854 AGAATCTCATCTCTCCCTGCTCTTGGACAGTGTGCTGCTGACAGAGGTGAGGATCA 2913
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2914 TCAGGCTCAGCATCTCAGCATCTAGGATGTGCTATGCTGATGAGTGTGACACTTTTGA 2973
1981 TCAGGCTCAGCATCTCAGCATCTAGGATGTGCTATGCTGATGAGTGTGACACTTTTGA 2040
2974 GAATCTGTTGATTTCCCGAGGCTTTCCCTCTCTTCCATGACAGGCTCACTATCAGCCCT 3033
2041 GAATCTGTTGATTTCCCGAGGCTTTCCCTCTCTTCCATGACAGGCTCACTATCAGCCCT 2100
3034 GAAAGTCCAACTTTCTGAACTTCCAGCAACCGTGTCTCTCTGCTGAGGCTGTTCATAGAG 3093

2101 GAAAGTCCAACTTTCTGAACTTTCCAGCACCGTCTGCTCTCTGCTGAGCTGTTCATAGAG 2160
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2161 CCACAGGACTGTAGCAGGATGACCTTTTCCAGCGCTGCTCTGAATCCAGACTGGT 2220
3154 GGCTGGAGGACAGCTCT 3170
2221 GGCTGGAGGACAGCTCT 2237
RESULT 3
US-09-861-101-3
; Sequence 3, Application US/09861101
; Publication No. US20030018984A1
; GENERAL INFORMATION:
; APPLICANT: COLEMAN, MICHAEL
; SCHWARTZ, ROBERT
; DEMAYO, FRANCESCO J.
; TITLE OF INVENTION: IGF-1 EXPRESSION SYSTEM AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,101
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,572
; FILING DATE: November 19, 1997
; APPLICATION NUMBER: 60/031,539
; FILING DATE: December 2, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/185-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-861-101-3
Query Match 40.9%; Score 2218; DB 3; Length 3599;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
3190 GAGCCAGGGAACAGCTCAGCTTTTGTCCCTTTAGTGAGGGTTAATTTGAGCTTGGCG 3249
3 GAGGGGGGGCCCGTACGCTTTTGTCCCTTTAGTGAGGGTTAATTTGAGCTTGGCG 62
3250 TAATCATGTGCATAGCTGTTTCTGTGTGAAATTTATCCGCTCACAATTCACACAC 3309
63 TAATCATGTGCATAGCTGTTTCTGTGTGAAATTTATCCGCTCACAATTCACACAC 122

Qy	3310	ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGCTTAACTCACA	3369
Db	123	ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGCTTAACTCACA	182
Qy	3370	TTAAATTCGGTTGGCTCAGCTGCCGCTTTCAGTTCGGGAAACCTGTGTCGCCAGCTGCAT	3429
Db	183	TTAAATTCGGTTGGCTCAGCTGCCGCTTTCAGTTCGGGAAACCTGTGTCGCCAGCTGCAT	242
Qy	3430	TAATGAATCGGCCAAACCGCGGGGAGAGCGGTTTGGTATTGGGGCTCTTCCGCTTCC	3489
Db	243	TAATGAATCGGCCAAACCGCGGGGAGAGCGGTTTGGTATTGGGGCTCTTCCGCTTCC	302
Qy	3490	TCGCTCACTGACTCGCTCGCTCGGTCGTTCCGCTCGCGAGCGGTATCAGTCTCACTCA	3549
Db	303	TCGCTCACTGACTCGCTCGCTCGGTCGTTCCGCTCGCGAGCGGTATCAGTCTCACTCA	362
Qy	3550	AAGCGGTAAATACGGTTATCCACAGAATCAGGGGATAAACGAGGAAAGACATGTGAGCA	3609
Db	363	AAGCGGTAAATACGGTTATCCACAGAATCAGGGGATAAACGAGGAAAGACATGTGAGCA	422
Qy	3610	AAAGGCCAGCAAAAGGCGCAGGAACCGGTAAAGAGCCGCTTGTCTGGCGTTTTTCCATAGG	3669
Db	423	AAAGGCCAGCAAAAGGCGCAGGAACCGGTAAAGAGCCGCTTGTCTGGCGTTTTTCCATAGG	482
Qy	3670	CTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCCG	3729
Db	483	CTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCCG	542
Qy	3730	ACAGGACTAATAAGATACGAGGCGTTTCCCCCTGGAGACTCCCTCGTCGCTCTCCGTTT	3789
Db	543	ACAGGACTAATAAGATACGAGGCGTTTCCCCCTGGAGACTCCCTCGTCGCTCTCCGTTT	602
Qy	3790	CCGACCCTGCGCTTACCGGATACCTCTCGCCCTTCTCCCTTCGGGAAACGCTGGCGCTT	3849
Db	603	CCGACCCTGCGCTTACCGGATACCTCTCGCCCTTCTCCCTTCGGGAAACGCTGGCGCTT	662
Qy	3850	TCTCATAGTCAACGCTGTAGTATCTCAGTTTCGGTGTAGTTCGTTTCGCTCAAAGCTGGGC	3909
Db	663	TCTCATAGTCAACGCTGTAGTATCTCAGTTTCGGTGTAGTTCGTTTCGCTCAAAGCTGGGC	722
Qy	3910	TGTTGTGACGAACCCCGCTTCAGCCGACCGCTGCGCCTTATCCGTTAACTATCGTCTT	3969
Db	723	TGTTGTGACGAACCCCGCTTCAGCCGACCGCTGCGCCTTATCCGTTAACTATCGTCTT	782
Qy	3970	GAGTCCAAACCCGGTAAGACACGACTTATCGCACTTCGCACATGGCAGCAGCACTGTTAAACAGGATT	4029
Db	783	GAGTCCAAACCCGGTAAGACACGACTTATCGCACTTCGCACATGGCAGCAGCACTGTTAAACAGGATT	842
Qy	4030	AGCAGAGCGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCTTAACCTACGCGC	4089
Db	843	AGCAGAGCGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCTTAACCTACGCGC	902
Qy	4090	TACACTAGAGAACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACTCTCGGAAAA	4149
Db	903	TACACTAGAGAACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACTCTCGGAAAA	962
Qy	4150	AGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCAACCGCTGGTAGCGGTGGTTTTTGGTT	4209
Db	963	AGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCAACCGCTGGTAGCGGTGGTTTTTGGTT	1022
Qy	4210	TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCTCTTTGATCTTTTCT	4269
Db	1023	TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCTCTTTGATCTTTTCT	1082
Qy	4270	ACGGGGTCTGACGCTCAGAGAACTCTGTCAAGAAGCGGATAGAGGCGATGCGCTGCGAA	4329
Db	1083	ACGGGGTCTGACGCTCAGAGAACTCTGTCAAGAAGCGGATAGAGGCGATGCGCTGCGAA	1142
Qy	4330	TCGGGAGCGCGATACCGTAAAGCAACGAGGAAGCGGTCAAGCCCATTCGCCGCCAAGCTCT	4389
Db	1143	TCGGGAGCGCGATACCGTAAAGCAACGAGGAAGCGGTCAAGCCCATTCGCCGCCAAGCTCT	1202

Qy	4390	TCAGCAATATCA CGGGTAGCCAA CGCTATATGCTCTGATAGCGGTCCGCCACACCCAGCCGG	4449
Db	1203	TCAGCAATATCA CGGGTAGCCAA CGCTATATGCTCTGATAGCGGTCCGCCACACCCAGCCGG	1262
Qy	4450	CCACAGTCGATGAATCCAGAAAAAGCGCCATTTTCACCATGATATTTCCGCCAAAGCAGGCA	4509
Db	1263	CCACAGTCGATGAATCCAGAAAAAGCGCCATTTTCACCATGATATTTCCGCCAAAGCAGGCA	1322
Qy	4510	TCGCCATGGGTCA CAGCAGAGATCCTCGCCGTGCGGCGATGCGCGCTTGAGCCTTGGCGAAC	4569
Db	1323	TOGCCATGGGTCA CAGCAGAGATCCTCGCCGTGCGGCGATGCGCGCTTGAGCCTTGGCGAAC	1382
Qy	4570	AGTTCCGCTCGCGGAGCCCTGATGCTCTTCGTCAGAGATCATCTCGATCGA CAAAGACCG	4629
Db	1383	AGTTCCGCTCGCGGAGCCCTGATGCTCTTCGTCAGAGATCATCTCGATCGA CAAAGACCG	1442
Qy	4630	GCTTCCATCCGAGTACGTGCTCGCTCGATCGGATGTTTTCGCTTGGTGGTCCGAATGGGCAG	4689
Db	1443	GCTTCCATCCGAGTACGTGCTCGCTCGATCGGATGTTTTCGCTTGGTGGTCCGAATGGGCAG	1502
Qy	4690	GTAGCCGGATCAAGCGTATCAGCGCGCGCATTTGCAATCAGCAATGATGGATATCTTCTCG	4749
Db	1503	GTAGCCGGATCAAGCGTATCAGCGCGCGCATTTGCAATCAGCAATGATGGATATCTTCTCG	1562
Qy	4750	GCAGGCAAGGTGAGATGACAGAGATCCTGCCCGGCACTTTCGCCCAATAGCAGCCAG	4809
Db	1563	GCAGGCAAGGTGAGATGACAGAGATCCTGCCCGGCACTTTCGCCCAATAGCAGCCAG	1622
Qy	4810	TCCCTTCCCGTTTCAGTGACAA CGTCAGACAGCTGCGCAAGAA CGCCCGTGGGCC	4869
Db	1623	TCCCTTCCCGTTTCAGTGACAA CGTCAGACAGCTGCGCAAGAA CGCCCGTGGGCC	1682
Qy	4870	AGCCA CAGATAGCCGCTGCTGCTGCTG CAGTT CATTCAGGCGACCGGACAGGTGGTC	4929
Db	1683	AGCCA CAGATAGCCGCTGCTGCTGCTG CAGTT CATTCAGGCGACCGGACAGGTGGTC	1742
Qy	4930	TTGAAAAAAGAACCGGGCGCCCTCGCTGCTGACAGCCGGAA CACGGCGGATCAGAGCAG	4989
Db	1743	TTGAAAAAAGAACCGGGCGCCCTCGCTGCTGACAGCCGGAA CACGGCGGATCAGAGCAG	1802
Qy	4990	CCGATTTGCTGTTGTGCCAGTCA TAGCGGAATAGCCTCTCCACCAAGCGGCGCGAGAA	5049
Db	1803	CCGATTTGCTGTTGTGCCAGTCA TAGCGGAATAGCCTCTCCACCAAGCGGCGCGAGAA	1862
Qy	5050	CCTCGGTGCAATCCATCTGTTCATCATCGAAACGATCCTCATCTGCTCTTTGATCA	5109
Db	1863	CCTCGGTGCAATCCATCTGTTCATCATCGAAACGATCCTCATCTGCTCTTTGATCA	1922
Qy	5110	GATCTTGATCCCTGCGCCATCAGATCCTTTGGCGGCAAGAACCATCCAGTTTACTTTG	5169
Db	1923	GATCTTGATCCCTGCGCCATCAGATCCTTTGGCGGCAAGAACCATCCAGTTTACTTTG	1982
Qy	5170	CAGGGCTTCCAACTTAC CAGAGGGCGCC CAGCTGGCAATTCGGTTCGCTGCTGCTGTC	5229
Db	1983	CAGGGCTTCCAACTTAC CAGAGGGCGCC CAGCTGGCAATTCGGTTCGCTGCTGCTGTC	2042
Qy	5230	CATAAAACCGCCAGTCTAGCAACTGTTGGAAAGGGCGATCGGTGCGGGGCTCTTCGCTA	5289
Db	2043	CATAAAACCGCCAGTCTAGCAACTGTTGGAAAGGGCGATCGGTGCGGGGCTCTTCGCTA	2102
Qy	5290	TTACGCCAGCTGGCGAAAGGGGATGTGTCGAAGGGGATTAAGTTGGGTAA CCGCAGGG	5349
Db	2103	TTACGCCAGCTGGCGAAAGGGGATGTGTCGAAGGGGATTAAGTTGGGTAA CCGCAGGG	2162
Qy	5350	TTTTTCCAGTCA CCAAGCTTGTAA AACCAGCGCCAGTCAA TTTGTAATACGACTCACTATAG	5409
Db	2163	TTTTTCCAGTCA CCAAGCTTGTAA AACCAGCGCCAGTCAA TTTGTAATACGACTCACTATAG	2222
Qy	5410	GGCGAAATTGGAGCT	5423
Db	2223	GGCGAAATTGGAGCT	2236

RESULT 4
US-10-798-896-2
; Sequence 2, Application US/10798896
; Publication No. US20050238624A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS, Inc.
; TITLE OF INVENTION: Insulin-Like Growth Factor ("IGF-I") Plasmid Mediated Supplementa
; FILE OF INVENTION: Therapeutic Applications
; FILE REFERENCE: 108328.00172 - AVSI-0034
; CURRENT APPLICATION NUMBER: US/10798,896
; CURRENT FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3803
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid sequence for the pAV2002 plasmid.
US-10-798-896-2

Query Match 40.9%; Score 2218; DB 9; Length 3803;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 3190 GAGCCAGGGAACAGCTCAGCTTTTGTCCCTTTAGTGAGGGTTAATTTTCGAGCTTGGCG 3249
DB 1570 GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTTCGAGCTTGGCG 1629
QY 3250 TAATCATGTCATAGCTGTTTCTGTGTGAATTTATCCGCTCACAATTCACACAAAC 3309
DB 1630 TAATCATGTCATAGCTGTTTCTGTGTGAATTTATCCGCTCACAATTTCCACACAAAC 1689
QY 3310 ATACGAGCCGGAAGCAATAAGTGTAAAGCTCGGGTGCCCTAATGAGTGAAGTAACTCACA 3369
DB 1690 ATACGAGCCGGAAGCAATAAGTGTAAAGCTCGGGTGCCCTAATGAGTGAAGTAACTCACA 1749
QY 3370 TTAATTTGCGTTGCGCTCACTGCCCGCTTTCAGTCCGGAAACCTGCTGTCGCAAGCTGCAT 3429
DB 1750 TTAATTTGCGTTGCGCTCACTGCCCGCTTTCAGTCCGGAAACCTGCTGTCGCAAGCTGCAT 1809
QY 3430 TAATGAATCGGCCAAACCGCGGGGAGAGGGCGTTTGGTATTTGGGCGCTCTTCGCTTCC 3489
DB 1810 TAATGAATCGGCCAAACCGCGGGGAGAGGGCGTTTGGTATTTGGGCGCTCTTCGCTTCC 1869
QY 3490 TCCTCACTCACTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3549
DB 1870 TCCTCACTCACTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1929
QY 3550 AAGCGGTTAATACGGTTATCCACAGAAATCAGGGGTAACCGCAGGAAAGAAACATGTGAGCA 3609
DB 1930 AAGCGGTTAATACGGTTATCCACAGAAATCAGGGGTAACCGCAGGAAAGAAACATGTGAGCA 1989
QY 3610 AAAGGCCAGAAAGCCAGGAACCGGTAAAGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3669
DB 1990 AAAGGCCAGAAAGCCAGGAACCGGTAAAGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2049
QY 3670 CTCGCGCCCTCAGCAGGATCAACAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
DB 2050 CTCGCGCCCTCAGCAGGATCAACAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCG 2109
QY 3730 ACAGGACTATAAAGATACCAAGGGGTTTCCCTCGGAGCTCCCTCGTGGCGCTCTCCTGTT 3789
DB 2110 ACAGGACTATAAAGATACCAAGGGGTTTCCCTCGGAGCTCCCTCGTGGCGCTCTCCTGTT 2169
QY 3790 CGACCCCTGCGCTTACCGGATACCTGTCGCTTCTCCCTTCGGAAGCGTGGCGCTT 3849
DB 2170 CGACCCCTGCGCTTACCGGATACCTGTCGCTTCTCCCTTCGGAAGCGTGGCGCTT 2229
QY 3850 TCCTCATGCTCAGCTGTAGGTATCTCAGTTCCGTTGAGTGTGCTTCCCTCCAGAGCTGGGC 3909
DB 2230 TCCTCATGCTCAGCTGTAGGTATCTCAGTTCCGTTGAGTGTGCTTCCCTCCAGAGCTGGGC 2289

QY 3910 TGTGTCCACGAACCCCCCGTTTCAGCCGCGCTTTCAGCCGCTTATCCCGTAATATTCGCTTT 3969
DB 2290 TGTGTCCACGAACCCCCCGTTTCAGCCGCGCTTTCAGCCGCTTATCCCGTAATATTCGCTTT 2349
QY 3970 GAGTCCAAACCCGTTAGACACGACTTATCGCCACTGCGACGACCACTGCTTACACAGATT 4029
DB 2350 GAGTCCAAACCCGTTAGACACGACTTATCGCCACTGCGACGACCACTGCTTACACAGATT 2409
QY 4030 AGCAGAGCAGAGTATGTCAGCGGCTGCTACAGAGTTCCTTGAAGTGGTGGCCCTAACTACGGC 4089
DB 2410 AGCAGAGCAGAGTATGTCAGCGGCTGCTACAGAGTTCCTTGAAGTGGTGGCCCTAACTACGGC 2469
QY 4090 TACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4149
DB 2470 TACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2529
QY 4150 AGAGTTGGTAGCTCTTGTATCCGCAACAAACCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4209
DB 2530 AGAGTTGGTAGCTCTTGTATCCGCAACAAACCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2589
QY 4210 TGCAAGCAGCAGATTACCGCGCAGAAAAAGAGATCTCAAGAAAGATCTCTTGTGATCTTTTCT 4269
DB 2590 TGCAAGCAGCAGATTACCGCGCAGAAAAAGAGATCTCTCAAGAAAGATCTCTTGTGATCTTTTCT 2649
QY 4270 ACGGGTCTGACGCTCAGAAAGAACTCGTCAAGAAAGGCGATAGAAAGCGATGCGCTGCGAA 4329
DB 2650 ACGGGTCTGACGCTCAGAAAGAACTCGTCAAGAAAGGCGATAGAAAGCGATGCGCTGCGAA 2709
QY 4330 TCGGAGCGCGATACCGTAAAGCAGGAAAGCGGTCAGCCCAATTCGCGCCCAAGCTCT 4389
DB 2710 TCGGAGCGCGATACCGTAAAGCAGGAAAGCGGTCAGCCCAATTCGCGCCCAAGCTCT 2769
QY 4390 TCAGCAATATCAGCGGTAGCCAAAGCTATGCTCTGATAGCGGTCCGCAACACCCAGCCGG 4449
DB 2770 TCAGCAATATCAGCGGTAGCCAAAGCTATGCTCTGATAGCGGTCCGCAACACCCAGCCGG 2829
QY 4450 CCACAGTGCATGATTCAGAAAGCGGCAATTTTCCACCATGATATTCGCAAGAGCGCA 4509
DB 2830 CCACAGTGCATGATTCAGAAAGCGGCAATTTTCCACCATGATATTCGCAAGAGCGCA 2889
QY 4510 TCGCATGGTTCAGCAGAGATCTCGCGTTCGGGCAATCGCGCTTTCAGCCCTGCGCAAC 4569
DB 2890 TCGCATGGTTCAGCAGAGATCTCGCGTTCGGGCAATCGCGCTTTCAGCCCTGCGCAAC 2949
QY 4570 AGTTTCGGCTGGCGAGCGCTGATGCTCTTCGTCAGATCATCTGATCGAAGACCG 4629
DB 2950 AGTTTCGGCTGGCGAGCGCTGATGCTCTTCGTCAGATCATCTGATCGAAGACCG 3009
QY 4630 GCTTCCATCCGAGTACGCTGCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCGAG 4689
DB 3010 GCTTCCATCCGAGTACGCTGCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCGAG 3069
QY 4690 GTAGCCGGATCAAGCGTATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4749
DB 3070 GTAGCCGGATCAAGCGTATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3129
QY 4750 GCAGGAGCAAGGTGAGATGACAGGAGATCTTCGCGCGCACTTCGCGCCATAGCAGCCAG 4809
DB 3130 GCAGGAGCAAGGTGAGATGACAGGAGATCTTCGCGCGCACTTCGCGCCATAGCAGCCAG 3189
QY 4810 TCCCTTCCCGCTTTCAGTGAACAGTTCGAGCAGCAGTTCGCGCAAGAAACGCGCTGCTGGCC 4869
DB 3190 TCCCTTCCCGCTTTCAGTGAACAGTTCGAGCAGCAGTTCGCGCAAGAAACGCGCTGCTGGCC 3249
QY 4870 AGCCAGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4929
DB 3250 AGCCAGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3309
QY 4930 TTGACAAAAAGAACCGGGCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4989
DB 3310 TTGACAAAAAGAACCGGGCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3369
QY 4990 CCGATTGCTGTTGTCGCCCATAGCCGAATAGCTCTTCCACCCCAAGCGCGCGAGAA 5049

Db 3370 CCAGTGTCTGTTGCGCCAGTCATAGCCGAATAGCTCTCCACCCAGCGCGGAGAA 3429
Qy 5050 CTGCGGTGCAATCACTTGTTCATCATCGAAAGCATCTCATCTGTCTCTTGATCA 5109
Db 3430 CTTGCGGTGCAATCACTTGTTCATCATCGAAAGCATCTCATCTGTCTCTTGATCA 3489
Qy 5110 GATCTTGATCCCTGCGCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
Db 3490 GATCTTGATCCCTGCGCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3549
Qy 5170 CAGGGCTTCCCAACTTACAGAGGGCGCCAGCTGGCAATTCGGTTCGCTTGTCTGTC 5229
Db 3550 CAGGGCTTCCCAACTTACAGAGGGCGCCAGCTGGCAATTCGGTTCGCTTGTCTGTC 3609
Qy 5230 CATAAACCCGCCAGCTAGCACTGTGTGGGAAGGGCGATCGGTGCGGGCTCTCTTCGCTA 5289
Db 3610 CATAAACCCGCCAGCTAGCACTGTGTGGGAAGGGCGATCGGTGCGGGCTCTCTTCGCTA 3669
Qy 5290 TTAGCCAGCTGCGGAAGGGGATGTCTGCAAGGCGATTAAGTTGGGTAAAGCCAGGG 5349
Db 3670 TTAGCCAGCTGCGGAAGGGGATGTCTGCAAGGCGATTAAGTTGGGTAAAGCCAGGG 3729
Qy 5350 TTTTCCAGTCACGACCTTGTAAACCGACGCCAGTCGAATTTGTAATACGACTCACTATAG 5409
Db 3730 TTTTCCAGTCACGACCTTGTAAACCGACGCCAGTCGAATTTGTAATACGACTCACTATAG 3789
Qy 5410 GCGCAATTGGAGCT 5423
Db 3790 GCGCAATTGGAGCT 3803

RESULT 5

US-09-861-101-2
; Sequence 2, Application US/09861101
; Publication No. US20030018984A1
; GENERAL INFORMATION:
; APPLICANT: COLEMAN, MICHAEL
; SCHWARTZ, ROBERT
; DEMAYO, FRANCESCO J.
; TITLE OF INVENTION: IGF-1 EXPRESSION SYSTEM AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: PASCSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861.101
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,572
; FILING DATE: November 19, 1997
; APPLICATION NUMBER: 60/031,539
; FILING DATE: December 2, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/185-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-101-2

Query Match 40.9%; Score 2215.8; DB 3; Length 3600;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3205 CTGAGCTTTTGTCCCTTTAGTCAGGGTTAAATTCGAGCTTGGCGTAAATCATCATGTCATAG 3264
Db 19 CCAGCTTTTGTCCCTTTAGTCAGGGTTAAATTCGAGCTTGGCGTAAATCATGTCATAG 78
Qy 3265 CTGTTTCTCTGTGAAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCCGGAAGC 3324
Db 79 CTGTTTCTCTGTGAAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCCGGAAGC 138
Qy 3325 ATAAAGTGAAGCTTGGGGTGCCTAATAGTGAAGTAACTCACTAATTAATTGCGTTCGCG 3384
Db 139 ATAAAGTGAAGCTTGGGGTGCCTAATAGTGAAGTAACTCACTAATTAATTGCGTTCGCG 198
Qy 3385 TCAGTCCCGCTTTCCAGTCGGGAAACCTGTGCGGAGCTGCATTAATGAATCGGCCAA 3444
Db 199 TCAGTCCCGCTTTCCAGTCGGGAAACCTGTGCGGAGCTGCATTAATGAATCGGCCAA 258
Qy 3445 CGCGCGGGAGAGCGGTTTGGCGTATTTGGCGGCTCTTCCGCTTCTCCGCTCACTGACTCG 3504
Db 259 CGCGCGGGAGAGCGGTTTGGCGTATTTGGCGGCTCTTCCGCTTCTCCGCTCACTGACTCG 318
Qy 3505 CTGCGCTCGGTCGTTCCGCTGCGGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGG 3564
Db 319 CTGCGCTCGGTCGTTCCGCTGCGGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGG 378
Qy 3565 TTATCCACAGAAATCAGGGGATACGAGGAAGCAATGTGAGCAAAAGCCGACAAAG 3624
Db 379 TTATCCACAGAAATCAGGGGATACGAGGAAGCAATGTGAGCAAAAGCCGACAAAG 438
Qy 3625 GCCAGGAACCGTAAAGGCGCGTGTCTGCGGCTTTTCCATAGGCTCCGCCCCCTGAC 3684
Db 439 GCCAGGAACCGTAAAGGCGCGTGTCTGCGGCTTTTCCATAGGCTCCGCCCCCTGAC 498
Qy 3685 GAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGA 3744
Db 499 GAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGA 558
Qy 3745 TACCAGGCTTTCCCGCTGGAAGCTCCCTGCGGCTCTCCTGTTCCGACCCCTGCGCTT 3804
Db 559 TACCAGGCTTTCCCGCTGGAAGCTCCCTGCGGCTCTCCTGTTCCGACCCCTGCGCTT 618
Qy 3805 ACCGATACCTGTCCGCTTTTCTCCCTTCGGAAGCGTGGCGCTTCTCTATAGTCAAGC 3864
Db 619 ACCGATACCTGTCCGCTTTTCTCCCTTCGGAAGCGTGGCGCTTCTCTATAGTCAAGC 678
Qy 3865 TGTAGGTATCTCAGTTCGCTGTTAGGTTCGCTTCCAAAGCTGGGCTGTGTGACAGAACCC 3924
Db 679 TGTAGGTATCTCAGTTCGCTGTTAGGTTCGCTTCCAAAGCTGGGCTGTGTGACAGAACCC 738
Qy 3925 CCGTTTCAGCCCGACCGCTTATCCGTTATCCGTTATCTGTTAGTCCAAACCCGTA 3984
Db 739 CCGTTTCAGCCCGACCGCTTATCCGTTATCTGTTAGTCCAAACCCGTA 798
Qy 3985 AGACACGACTTATCGCCACTGGCAGCAGCCACTGTTAAAGGATTAGCAGAGCGAGTAT 4044
Db 799 AGACACGACTTATCGCCACTGGCAGCAGCCACTGTTAAAGGATTAGCAGAGCGAGTAT 858
Qy 4045 GTAGGCGGTCTACAGAGTCTTTGAAGTGTGGCTTAACCTACGCGCTACACTAGAAAGACA 4104
Db 859 GTAGGCGGTCTACAGAGTCTTTGAAGTGTGGCTTAACCTACGCGCTACACTAGAAAGACA 918

QY 4105 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGGTAGCTCT 4164
DB 919 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGGTAGCTCT 978
QY 4165 TGATCCGGCAAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAGCAGCAGATT 4224
DB 979 TGATCCGGCAAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAGCAGCAGATT 1038
QY 4225 ACCGCGAGAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGGTCTGACGCT 4284
DB 1039 ACCGCGAGAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGGTCTGACGCT 1098
QY 4285 CAGAGAATCTGTCAGAGAGCGGATAGAGCGGATCGCTGCGAATCGGAGCGGCGATA 4344
DB 1099 CAGAGAATCTGTCAGAGAGCGGATAGAGCGGATCGCTGCGAATCGGAGCGGCGATA 1158
QY 4345 CCGTAAGACGAGGAGCGGTGAGCCCATTCGCGCCAGCTCTTCAGGCAATATCACGG 4404
DB 1159 CCGTAAGACGAGGAGCGGTGAGCCCATTCGCGCCAGCTCTTCAGGCAATATCACGG 1218
QY 4405 GTAGCCAAAGCGTATGTCCTGATAGCGGTCCGCCACACCGCGGCCACAGTCGATGAAT 4464
DB 1219 GTAGCCAAAGCGTATGTCCTGATAGCGGTCCGCCACACCGCGGCCACAGTCGATGAAT 1278
QY 4465 CCAGAAAAAGCGGCAATTTTCCACCATGATATTCGCAAGCAGGCATCGCCATGGGTACG 4524
DB 1279 CCAGAAAAAGCGGCAATTTTCCACCATGATATTCGCAAGCAGGCATCGCCATGGGTACG 1338
QY 4525 ACAGATCTCGCGCTCGGCGATGCGGCTTGAGCTGCGCAACAGTTGCGGTGCGGCG 4584
DB 1339 ACAGATCTCGCGCTCGGCGATGCGGCTTGAGCTGCGCAACAGTTGCGGTGCGGCG 1398
QY 4585 AGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTCCATCCAGTA 4644
DB 1399 AGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTCCATCCAGTA 1458
QY 4645 CGTGCTCGCTCGATGCGGATGTTTCGCTGATGTCGAATGGGCGAGTAGCGGATCAAGC 4704
DB 1459 CGTGCTCGCTCGATGCGGATGTTTCGCTGATGTCGAATGGGCGAGTAGCGGATCAAGC 1518
QY 4705 GTATGAGCGCGCGATGATGATCAGCCATGATGATGATCTTTCGCGAGGAGCAAGTGA 4764
DB 1519 GTATGAGCGCGCGATGATGATCAGCCATGATGATGATCTTTCGCGAGGAGCAAGTGA 1578
QY 4765 GATGACAGAGATCTGCGCCGCGCATTCGCCCAATAGCAGCAGTCCCTTCCGCTTCA 4824
DB 1579 GATGACAGAGATCTGCGCCGCGCATTCGCCCAATAGCAGCAGTCCCTTCCGCTTCA 1638
QY 4825 GTGACAACTCGACACAGCTGCGCAAGGAACGCCCGTGTGGCGAGCCACGATAGCCGC 4884
DB 1639 GTGACAACTCGACACAGCTGCGCAAGGAACGCCCGTGTGGCGAGCCACGATAGCCGC 1698
QY 4885 GTGCTCTGCTGCTGAGTTCAATTCAGGCGACCGGACAGTTCGCTTGAACAAAGAAC 4944
DB 1699 GTGCTCTGCTGCTGAGTTCAATTCAGGCGACCGGACAGTTCGCTTGAACAAAGAAC 1758
QY 4945 GGGCGCCCTGCGCTGACAGCGGGAACACGGCGGCGATCAGAGCAGCGGATGCTGTTGT 5004
DB 1759 GGGCGCCCTGCGCTGACAGCGGGAACACGGCGGCGATCAGAGCAGCGGATGCTGTTGT 1818
QY 5005 GCCAGTCTAGCCGAATAGCTCTCCACCAAGCGGCGGAGAACCTCGTGCAATCA 5064
DB 1819 GCCAGTCTAGCCGAATAGCTCTCCACCAAGCGGCGGAGAACCTCGTGCAATCA 1878
QY 5065 TCTTGTTCATATGCGAAACGATCTCTGCTCTTGTATCAGATCTTGATCCCTG 5124
DB 1879 TCTTGTTCATATGCGAAACGATCTCTGCTCTTGTATCAGATCTTGATCCCTG 1938
QY 5125 CGCATCAGATCTTGGCGCAAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAACC 5184
DB 1939 CGCATCAGATCTTGGCGCAAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAACC 1998

RESULT 6

US-10-281-067B-26
; Sequence 26, Application US/10281067B
; Publication No. US20040138111A1
; GENERAL INFORMATION:

; APPLICANT: Baylor College of Medicine

; TITLE OF INVENTION: A COMPOSITION AND METHOD TO ALTER LEAN BODY MASS AND BOND PROPERT

; FILE REFERENCE: 108328.00071 - AVSI-0008

; CURRENT APPLICATION NUMBER: US/10/281,067B

; CURRENT FILING DATE: 2002-10-25

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 26

; LENGTH: 3558

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: Sequence for the inducible pGR174 containing GHRH.
US-10-281-067B-26

Query Match 40.8%; Score 2211.6; DB 7; Length 3558;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2217; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3190 GAGCCAGGAGCAAGCTCAGCTTTTGTCCCTTTAGTGAGGGTTAATTTCCAGCTTTGGCG 3249
DB 1200 GAGGGGGGGCCCGTACCAGCTTTTGTCCCTTTAGTGAGGGTTAATTTCCAGCTTTGGCG 1259
QY 3250 TAAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCAAAATTCACACAAC 3309
DB 1260 TAAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCAAAATTCACACAAC 1319
QY 3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCTTGGGGTCCCTAATGATGAGCTAACTCACA 3369
DB 1320 ATACGAGCCGGAAGCATAAAGTGTAAAGCTTGGGGTCCCTAATGATGAGCTAACTCACA 1379
QY 3370 TTAATTTGCGTTCGCTCACTGCGCGCTTTCCAGTTCGGGAAACCTGTCGTCAGAGTGCAT 3429
DB 1380 TTAATTTGCGTTCGCTCACTGCGCGCTTTCCAGTTCGGGAAACCTGTCGTCAGAGTGCAT 1439
QY 3430 TAAATGATCGGCAACCGCGCGGGAGAGCGGTTTTCGTTATTTGGGCGCTCTTCCGCTTCC 3489
DB 1440 TAAATGATCGGCAACCGCGCGGGAGAGCGGTTTTCGTTATTTGGGCGCTCTTCCGCTTCC 1499
QY 3490 TCGCTCACTGACTCGTTCGCTCGCTTCGCTTCGCTTCGCGGAGCGGTATCAGCTCACTCA 3549
DB 1500 TCGCTCACTGACTCGTTCGCTCGCTTCGCTTCGCTTCGCGGAGCGGTATCAGCTCACTCA 1559
QY 3550 AAGGCGGTAAATACGGTTATTCACAGAAATCAAGGAGTAAACGAGAAAGAACATGTGAGCA 3609
DB 1560 AAGGCGGTAAATACGGTTATTCACAGAAATCAAGGAGTAAACGAGAAAGAACATGTGAGCA 1619
QY 3610 AAGGCGCAGCAAAAGCCAGGAAACCGTAAAAAGCCGCTTGTGCTGCGTTTTTCCATAGG 3669
DB 1620 AAGGCGCAGCAAAAGCCAGGAAACCGTAAAAAGCCGCTTGTGCTGCGTTTTTCCATAGG 1679

Qy	3670	CTCGGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCG	3729
Db	1680	CTCGGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCG	1739
Qy	3730	ACAGGACTATAAGATACAGGGGTTTCCCCCTGGAAAGCTCCCTCGTGGCTCTCTGTT	3789
Db	1740	ACAGGACTATAAGATACAGGGGTTTCCCCCTGGAAAGCTCCCTCGTGGCTCTCTGTT	1799
Qy	3790	CCGACCTCGCGCTTACGGATACCTGTGCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT	3849
Db	1800	CCGACCTCGCGCTTACGGATACCTGTGCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT	1859
Qy	3850	TCTCATAGCTCAGCTCTAGGTATCTCAGTTCCGTTGAGTTCGTTCCCTCAAGCTGGGC	3909
Db	1860	TCTCATAGCTCAGCTCTAGGTATCTCAGTTCCGTTGAGTTCGTTCCCTCAAGCTGGGC	1919
Qy	3910	TGTGTGCAAGAACCCCGGTTCAAGCCGACCGCTGGCGCTTATCCGGTAACATATGCTTT	3969
Db	1920	TGTGTGCAAGAACCCCGGTTCAAGCCGACCGCTGGCGCTTATCCGGTAACATATGCTTT	1979
Qy	3970	GAGTCCAAACCGGTAAAGACAGACTTATCCGCACTGGCAGCAGCCACTGCTAACAGATT	4029
Db	1980	GAGTCCAAACCGGTAAAGACAGACTTATCCGCACTGGCAGCAGCCACTGCTAACAGATT	2039
Qy	4030	AGCAGCGCAGGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC	4089
Db	2040	AGCAGCGCAGGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC	2099
Qy	4090	TACACTAGAAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTTCGAAAA	4149
Db	2100	TACACTAGAAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTTCGAAAA	2159
Qy	4150	AGAGTTGGTAGCTTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTGT	4209
Db	2160	AGAGTTGGTAGCTTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTGT	2219
Qy	4210	TGCAAGCAGCAGATTACCGCCAGAAAAAAGGATCTCAAGAGATCCCTTTGATCTTTTCT	4269
Db	2220	TGCAAGCAGCAGATTACCGCCAGAAAAAAGGATCTCAAGAGATCCCTTTGATCTTTTCT	2279
Qy	4270	ACGGGCTCTGACGCTCAGAGAACTCGTCAAGAGCGGATAGAGGCGATGCGCTGCGAA	4329
Db	2280	ACGGGCTCTGACGCTCAGAGAACTCGTCAAGAGCGGATAGAGGCGATGCGCTGCGAA	2339
Qy	4330	TGGGAGGGGGATACCGTTAAACAGAGAGCGGTACGCCATTCGCGCGCCAGCTCT	4389
Db	2340	TGGGAGGGGGATACCGTTAAACAGAGAGCGGTACGCCATTCGCGCGCCAGCTCT	2399
Qy	4390	TCAGCAATACAGGGTAGCCACGCTATGTCTGATAGCGGTCCGCCACACCCAGCCGG	4449
Db	2400	TCAGCAATACAGGGTAGCCACGCTATGTCTGATAGCGGTCCGCCACACCCAGCCGG	2459
Qy	4450	CCAGTTCGATGAATCCAGAAAAAGCGCCATTTTCCACCATGATATTTCGGCAAGCAGCA	4509
Db	2460	CCAGTTCGATGAATCCAGAAAAAGCGCCATTTTCCACCATGATATTTCGGCAAGCAGCA	2519
Qy	4510	TGCGCATGGGTACGACGAGATCTTCGCGGTGGGCAATGCGCGCTTTGAGCCTTGGGAAC	4569
Db	2520	TGCGCATGGGTACGACGAGATCTTCGCGGTGGGCAATGCGCGCTTTGAGCCTTGGGAAC	2579
Qy	4570	AGTTCCGCTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTTCATCGACAGACCG	4629
Db	2580	AGTTCCGCTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTTCATCGACAGACCG	2639
Qy	4630	GCTTCCATCCGAGTACGTGCTCGATCGATCGATGATGTTTCGCTTGGTGGTCCGATGGGCG	4689
Db	2640	GCTTCCATCCGAGTACGTGCTCGATCGATCGATGATGTTTCGCTTGGTGGTCCGATGGGCG	2699
Qy	4690	GTAGCCGGATCAAGCGTATGAGCCCGCGCATTCGATCAGCCATGATGGATCTTTCTCG	4749
Db	2700	GTAGCCGGATCAAGCGTATGAGCCCGCGCATTCGATCAGCCATGATGGATCTTTCTCG	2759

Qy	4750	GCAGGACGAAGGTGAGATGACAGGAGATCCTGCCCGGCACATTCGCGCCCAATAGCAGCCAG	4809
Db	2760	GCAGGACGAAGGTGAGATGACAGGAGATCCTGCCCGGCACATTCGCGCCCAATAGCAGCCAG	2819
Qy	4810	TCCCTTCCCGCTTCAGTGTGACCAAGTCGCGACACAGCTCCGCAAGGAACGCCGCTCGTGGCC	4869
Db	2820	TCCCTTCCCGCTTCAGTGTGACCAAGTCGCGACACAGCTCCGCAAGGAACGCCGCTCGTGGCC	2879
Qy	4870	AGCCACGATAGCCGCGTGCCTCGTCTGAGTTCATTTCAGGGCACCCGACAGGTCGGTC	4929
Db	2880	AGCCACGATAGCCGCGTGCCTCGTCTGAGTTCATTTCAGGGCACCCGACAGGTCGGTC	2939
Qy	4930	TTGACAAAAAGAAACCGGGCGCCCTCGCTGTGACAGCCGGAAACACGGCGCGCATCAGAGCAG	4989
Db	2940	TTGACAAAAAGAAACCGGGCGCCCTCGCTGTGACAGCCGGAAACACGGCGCGCATCAGAGCAG	2999
Qy	4990	CCGATTGTCTGTTGTGCCAGTCAATAGCCGGAATAGCCTCTCCACCCCAAGCGGCCGGAGAA	5049
Db	3000	CCGATTGTCTGTTGTGCCAGTCAATAGCCGGAATAGCCTCTCCACCCCAAGCGGCCGGAGAA	3059
Qy	5050	CCTGCGTGCAAATCCATCTTGTTCAATCATCGGAAAACGATCCTCATCTCTGTCTCTTGATCA	5109
Db	3060	CCTGCGTGCAAATCCATCTTGTTCAATCATCGGAAAACGATCCTCATCTCTGTCTCTTGATCA	3119
Qy	5110	GATCTTGATCCCCCTGGCCATCAGATCCTTTGGCGGCAAGAACCCATCCAGTTTACTTTG	5169
Db	3120	GATCTTGATCCCCCTGGCCATCAGATCCTTTGGCGGCAAGAACCCATCCAGTTTACTTTG	3179
Qy	5170	CAGGGCTTCCCAACCTTACACAGAGGCGCCCCAGCTGGGCAATTCGCGTTTCGTTGCTGTC	5229
Db	3180	CAGGGCTTCCCAACCTTACACAGAGGCGCCCCAGCTGGGCAATTCGCGTTTCGTTGCTGTC	3239
Qy	5230	CATATAACCCGCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGGGGGCTCTTCGCTA	5289
Db	3240	CATATAACCCGCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGGGGGCTCTTCGCTA	3299
Qy	5290	TTACGCCAGCTGGCGAAAGGGCGATGTGTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGG	5349
Db	3300	TTACGCCAGCTGGCGAAAGGGCGATGTGTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGG	3359
Qy	5350	TTTTTCCCAGTCACGACGTTGTGTAAAACGACGGCCAGTGAAATTGTAATACGACTCATTATAG	5409
Db	3360	TTTTTCCCAGTCACGACGTTGTGTAAAACGACGGCCAGTGAAATTGTAATACGACTCATTATAG	3419
Qy	5410	GGCGAATT 5417	
Db	3420	GGCGAATT 3427	


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Db 3360 TTTTCCAGTCACGAGCTGTAAACGAGCGCCAGTGAATTTGATAGGACTCACTATAG 3419
Qy 5410 GCGCAATT 5417
Db 3420 GCGCAATT 3427

RESULT 8
US-10-021-403A-10
; Sequence 10, Application US/10021403A
; Publication No. US20030074679A1
; GENERAL INFORMATION:
; APPLICANT: Advise
; TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhance
; TITLE OF INVENTION: Growth in Offspring
; FILE REFERENCE: HO-P02021US/100021476/OTA 00-91
; CURRENT APPLICATION NUMBER: US/10/021.403A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/255,021
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 2192
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is a plasmid vector comprising a pVC0289 backbone
US-10-021-403A-10

Query Match 39.8%; Score 2160; DB 5; Length 2192;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3190 GAGCCAGCGAACAAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTGCGAGCTTGCGG 3249
Db 17 GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTGCGAGCTTGCGG 76

Qy 3250 TAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCGGCTCAAAATTCACACAAC 3309
Db 77 TAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCGGCTCAAAATTCACACAAC 136

Qy 3310 ATAGGCGCGGAGCATAAAGTGAAGCCCTGGGGTGCCTAAATGAGTGAGTCACTACTACA 3369
Db 137 ATAGGCGCGGAGCATAAAGTGAAGCCCTGGGGTGCCTAAATGAGTGAGTCACTACTACA 196

Qy 3370 TTAATTGCGTTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTGTCGCCAGCTGCAT 3429
Db 197 TTAATTGCGTTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTGTCGCCAGCTGCAT 256

Qy 3430 TAATGAATTCGGCCAAACGCGGGGAGAGGGCGTTTGGGTATTTGGGGCGCTCTTCGCGTTCC 3489
Db 257 TAATGAATTCGGCCAAACGCGGGGAGAGGGCGTTTGGGTATTTGGGGCGCTCTTCGCGTTCC 316

Qy 3490 TCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
Db 317 TCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA 376

Qy 3550 AAGCGCGTAAATPACGGTTATCCACAGAAATCAGGGGATAACCGAGGAAAGAAATCATGTAGCA 3609
Db 377 AAGCGCGTAAATPACGGTTATCCACAGAAATCAGGGGATAACCGAGGAAAGAAATCATGTAGCA 436

Qy 3610 AAAGCCAGCAAAAGGCCAGGAAACCGTTAAAGCCCGGTTCGTTGGGTTTTCATAGG 3669
Db 437 AAAGCCAGCAAAAGGCCAGGAAACCGTTAAAGCCCGGTTCGTTGGGTTTTCATAGG 496

Qy 3670 CTCCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGCGGAAACCCG 3729
Db 497 CTCCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGCGGAAACCCG 556

Qy 3730 ACAGGACTATAAAGATACAGGCGGTTTCCCTCGGAAGCTCCCTCGTGCCTCTCTGTT 3789
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Db 557 ACAGGACTATAAAGATACCAAGGCGTTTCCCTTGGAAAGCTCCCTCGTGCCTCTCTGTT 616
Qy 3790 CCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
Db 617 CCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT 676
Qy 3850 TCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGGTTCGCTTCAAGCTGGGC 3909
Db 677 TCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGGTTCGCTTCAAGCTGGGC 736
Qy 3910 TGTGTGACGAACCCCGCTTACCGGACCGCTGCGCTTATCCCGTAACTATCGTCTT 3969
Db 737 TGTGTGACGAACCCCGCTTACCGGACCGCTGCGCTTATCCCGTAACTATCGTCTT 796
Qy 3970 GAGTCCAAACCGGTAAAGACAGCACTTATCGCACTGSCAGCAGCACTGTGTAAACAGATT 4029
Db 797 GAGTCCAAACCGGTAAAGACAGCACTTATCGCACTGSCAGCAGCACTGTGTAAACAGATT 856
Qy 4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGC 4089
Db 857 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGC 916
Qy 4090 TACACTAGAAAGAACAGATTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTTCGGA 4149
Db 917 TACACTAGAAAGAACAGATTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTTCGGA 976
Qy 4150 AGAGTTGGTAGCTCTTGATCCGCAACAAACACACCGCTGCTAGCGGTGGTTTTTTGTT 4209
Db 977 AGAGTTGGTAGCTCTTGATCCGCAACAAACACACCGCTGCTAGCGGTGGTTTTTTGTT 1036
Qy 4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTCT 4269
Db 1037 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTCT 1096
Qy 4270 ACGGGCTCTGAGCTCAGAAAGAACTCGTCAAGAAAGCGATAGAAGGCGATGCGCTCGAA 4329
Db 1097 ACGGGCTCTGAGCTCAGAAAGAACTCGTCAAGAAAGCGATAGAAGGCGATGCGCTCGAA 1156
Qy 4330 TCGGAGCGGATACCGTAAAGCAGGAGAGCGGTGAGCCCACTTCGCCCAAGCTCT 4389
Db 1157 TCGGAGCGGATACCGTAAAGCAGGAGAGCGGTGAGCCCACTTCGCCCAAGCTCT 1216
Qy 4390 TCAGCAATATCAGGGTAGCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCGG 4449
Db 1217 TCAGCAATATCAGGGTAGCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCGG 1276
Qy 4450 CCAAGTCGATGAATCAGAAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCA 4509
Db 1277 CCAAGTCGATGAATCAGAAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCA 1336
Qy 4510 TCGCCATGGGTACGAGAGATCCTCGCGTCCGGCATGCGGCTTGAGCTTCGGCAAGC 4569
Db 1337 TCGCCATGGGTACGAGAGATCCTCGCGTCCGGCATGCGGCTTGAGCTTCGGCAAGC 1396
Qy 4570 AGTTTCGGCTCGCGAGCCCTCTGATGCTCTTTCGTCAGATCATCTGATCGCAAGACCG 4629
Db 1397 AGTTTCGGCTCGCGAGCCCTCTGATGCTCTTTCGTCAGATCATCTGATCGCAAGACCG 1456
Qy 4630 GCTTCATTCGAGTACGCTCGCTCGATGGATGTTTCGTTGGTGGTGAATGGGCGAG 4689
Db 1457 GCTTCATTCGAGTACGCTCGCTCGATGGATGTTTCGTTGGTGGTGAATGGGCGAG 1516
Qy 4690 GTAGCCCGATCAAGCGTATGCGAGCCCGCATTCGATCAGCCATGATGATCTTTCTCG 4749
Db 1517 GTAGCCCGATCAAGCGTATGCGAGCCCGCATTCGATCAGCCATGATGATCTTTCTCG 1576
Qy 4750 GCAGGACCAAGGTGAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCCAG 4809
Db 1577 GCAGGACCAAGGTGAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCCAG 1636
Qy 4810 TCCCTTCGCGCTTCAGTGACAACTCGAGCAGCAGCTGGGCAAGGAAACGCCCGCTCGTGCC 4869
Db 1637 TCCCTTCGCGCTTCAGTGACAACTCGAGCAGCAGCTGGGCAAGGAAACGCCCGCTCGTGCC 1696
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; OTHER INFORMATION: smid.
us-10-395-709-13

Query Match 39.8%; Score 2160; DB 7; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3190 GAGCAGGGAACAAGCTCAGCTTTGTTGCTTTAGTGAGGGTTAAATTCAGAGCTGGCG 3249
Db |||||
Qy 1359 GAGGGGGGGCGGTACAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCAGAGCTGGCG 1418
Db |||||
Qy 3250 TAATCATGCTCATAGCTGTTTCTGTGTAATTTGTTATCGCTCACAATTCACACAAC 3309
Db |||||
Qy 1419 TAATCATGCTCATAGCTGTTTCTGTGTAATTTGTTATCGCTCACAATTTCCACAAC 1478
Db |||||
Qy 3310 ATACGAGCCGGAACATAAAGTGTAAAGCTTGGGGTGCCTAAATGAGTGAGCTAACTCACA 3369
Db |||||
Qy 1479 ATACGAGCCGGAACATAAAGTGTAAAGCTTGGGGTGCCTAAATGAGTGAGCTAACTCACA 1538
Db |||||
Qy 3370 TTAATTGCGTTGCGCTCACTGCCGCTTTCCAGTCGGGAACCTGTCGTCCAGCTGCAT 3429
Db |||||
Qy 1539 TTAATTGCGTTGCGCTCACTGCCGCTTTCCAGTCGGGAACCTGTCGTCCAGCTGCAT 1598
Db |||||
Qy 3430 TAATGAATCGCCCAACCGCGGGGAGAGCGGTTTGGTATTTGGGCGCTCTTCGCTTCC 3489
Db |||||
Qy 1599 TAATGAATCGCCCAACCGCGGGGAGAGCGGTTTGGTATTTGGGCGCTCTTCGCTTCC 1658
Db |||||
Qy 3490 TCGCTCACTGACTCGCTGCGCTGCTTGGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
Db |||||
Qy 1659 TCGCTCACTGACTCGCTGCGCTGCTTGGCTGCGGCGAGCGGTATCAGCTCACTCA 1718
Db |||||
Qy 3550 AAGCGGTAAATACGGTTATCCACAGATCAGGGGATAACCGAGGAAGAAATGTGAGCA 3609
Db |||||
Qy 1719 AAGCGGTAAATACGGTTATCCACAGATCAGGGGATAACCGAGGAAGAAATGTGAGCA 1778
Db |||||
Qy 3610 AAGGCCAGCAAAAGGCCAGAACCGTAAAGGCCGCTTGGTGGGTTTTCATAGG 3669
Db |||||
Qy 1779 AAGGCCAGCAAAAGGCCAGAACCGTAAAGGCCGCTTGGTGGGTTTTCATAGG 1838
Db |||||
Qy 3670 CTCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGCGGAACCCG 3729
Db |||||
Qy 1839 CTCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGCGGAACCCG 1898
Db |||||
Qy 3730 ACAGGACTATAAAGATACCAAGGGTTTCCCGCTGGAGCTCCCTCGTGCCTCTCTCTGT 3789
Db |||||
Qy 1899 ACAGGACTATAAAGATACCAAGGGTTTCCCGCTGGAGCTCCCTCGTGCCTCTCTCTGT 1958
Db |||||
Qy 3790 CCGACCTGCGCTTACCGGATACCTGTCGCTTTCTCCCTCGGGAAAGCGTGGCGTT 3849
Db |||||
Qy 1959 CCGACCTGCGCTTACCGGATACCTGTCGCTTTCTCCCTCGGGAAAGCGTGGCGTT 2018
Db |||||
Qy 3850 TCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGTCTGCTCCTCAAGCTGGGC 3909
Db |||||
Qy 2019 TCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGTCTGCTCCTCAAGCTGGGC 2078
Db |||||
Qy 3910 TGTGTGCAAGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTT 3969
Db |||||
Qy 2079 TGTGTGCAAGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTT 2138
Db |||||
Qy 3970 GAGTCCAAACCGGTAAAGACAGCTTATCCGCACTGCGAGCGCACTGTGTAAACAGATT 4029
Db |||||
Qy 2139 GAGTCCAAACCGGTAAAGACAGCTTATCCGCACTGCGAGCGCACTGTGTAAACAGATT 2198
Db |||||
Qy 4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCTTAACACGGC 4089
Db |||||
Qy 2199 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCTTAACACGGC 2258
Db |||||
Qy 4090 TACATAGAAAGACAGATTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACTTCGGAATA 4149
Db |||||
Qy 2259 TACATAGAAAGACAGATTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACTTCGGAATA 2318
Db |||||
Qy 4150 AGAGTTGGTAGCTTCTGATCCGGCAACAAACCAACCGCTGGTAGCGGTGTTTTTTGTT 4209
Db |||||

Db 2319 AGAGTTGGTAGCTTCTGATCCGGCAACAAACCAACCGCTGGTAGCGGTGTTTTTTGTT 2378
Qy |||||
Db 4210 TGCAAGCAGCAGATTACCGCGCAGAAAAAAGGATCTCAAGAAAGATCTTTGATCTTTTCT 4269
Qy |||||
Db 2379 TGCAAGCAGCAGATTACCGCGCAGAAAAAAGGATCTCAAGAAAGATCTTTGATCTTTTCT 2438
Qy |||||
Db 4270 ACGGGTCTGACCTCAGAAAGAACTGCTCAAGAAAGGCGATAGAAAGGCGATCGCTCGAA 4329
Qy |||||
Db 2439 ACGGGTCTGACCTCAGAAAGAACTGCTCAAGAAAGGCGATAGAAAGGCGATCGCTCGAA 2498
Qy |||||
Db 4330 TCGGGAGCGCGATACCGTAAAGCAGGAAAGCGGTCAAGCCATTCGCGCCCAAGCTCT 4389
Qy |||||
Db 2499 TCGGGAGCGCGATACCGTAAAGCAGGAAAGCGGTCAAGCCATTCGCGCCCAAGCTCT 2558
Qy |||||
Db 4390 TCAGCAATATCAGCGGTAGCAACGCTATGCTCTGATAGCGGTCCGCGCACACCCAGCGCG 4449
Qy |||||
Db 2559 TCAGCAATATCAGCGGTAGCAACGCTATGCTCTGATAGCGGTCCGCGCACACCCAGCGCG 2618
Qy |||||
Db 4450 CCAAGTCTGATGATCCAGAAAAAGCGGCTCAATTTTCCACATGATATTCGGCAAGCAGCA 4509
Qy |||||
Db 2619 CCAAGTCTGATGATCCAGAAAAAGCGGCTCAATTTTCCACATGATATTCGGCAAGCAGCA 2678
Qy |||||
Db 4510 TCGCCATGGGTACAGCAGATCCTCGCGTCCGGGATCGCGCTTGAGCCTGGCGAAC 4569
Qy |||||
Db 2679 TCGCCATGGGTACAGCAGATCCTCGCGTCCGGGATCGCGCTTGAGCCTGGCGAAC 2738
Qy |||||
Db 4570 AGTTCCGCTGGCGAGCGCCCTGATGCTCTTCCGTCAGATCATCTCTGATCAAGACCG 4629
Qy |||||
Db 2739 AGTTCCGCTGGCGAGCGCCCTGATGCTCTTCCGTCAGATCATCTCTGATCAAGACCG 2798
Qy |||||
Db 4630 GCTTCCATCCGAGTACGCTGCTCGATGCGATGTTTCCGTTGGTGGTGGTGGGAG 4699
Qy |||||
Db 2799 GCTTCCATCCGAGTACGCTGCTCGATGCGATGTTTCCGTTGGTGGTGGTGGGAG 2858
Qy |||||
Db 4690 GTAGCCGATCAGCGCTATGCGCGCGCTGATGCGATGATGCGATGATGCGATGATGCG 4749
Qy |||||
Db 2859 GTAGCCGATCAGCGCTATGCGCGCGCTGATGCGATGATGCGATGATGCGATGATGCG 2918
Qy |||||
Db 4750 GCAGGAGCAGGTGAGATGACAGGAGATCTCTGCGCGCGCTTCCGCGCAATAGCAGCAG 4809
Qy |||||
Db 2919 GCAGGAGCAGGTGAGATGACAGGAGATCTCTGCGCGCGCTTCCGCGCAATAGCAGCAG 2978
Qy |||||
Db 4810 TCCTTTCCGCTTTCAGTGACAGCTCGAGCAGCTGCGCAAGGAAACCGCGCTGGTGGCC 4869
Qy |||||
Db 2979 TCCTTTCCGCTTTCAGTGACAGCTCGAGCAGCTGCGCAAGGAAACCGCGCTGGTGGCC 3038
Qy |||||
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Qy |||||
Db 3039 AGCCAGATAGCGCGCTGCTGCTCTGAGTTCATTCAGGGCAACCGGACAGGTGCGTC 3098
Qy |||||
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Qy |||||
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Qy |||||
Db 4990 CCGATTGTCTGTTGCTGCCCATAGCGGAAATAGCTCTTCCACCCAGCGCGGAGAA 5049
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US-10-395-709-14
; Sequence 14, Application US/10395709
; Publication No. US20040014645A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL
; TITLE OF INVENTION: GLUTAMATE ("PLG") SYSTEM
; FILE REFERENCE: 108328.00115 - AVSI-0021P1
; CURRENT APPLICATION NUMBER: US/10/395,709
; CURRENT FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the operatively linked components of the 15/27/28 GH
; OTHER INFORMATION: RH plasmid.
US-10-395-709-14

Query Match 39.8%; Score 2160; DB 7; Length 3534;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 3250 TAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAAC 3309
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QY 4210 TGCAAGCAGCAGATTACGCGCAGAAAGAGTCTCAAGAAAGTCTCAAGAAAGTCTTGTGATCTTTCT 4269
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Db 2499 TCGGAGCGCGGATACCGTAAAGCAGAGGAGGCTCAGCCCTTTCGCCGCCAAGCTCT 2558
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Db 2559 TCAGCAATATCAGCGGTAGCCAAACGCTATCTCTGATAGCGGTCCGCGCACACCCAGCGG 2618
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QY 4930 TTGACAAAAGAACCGGCGCCCTGCGCTGACAGCGGAAACACGCGGGCATCAGAGCAG 4989
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QY 4990 CCGATTGTCTGTGTGCGCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGCGAGAA 5049
Db 3159 CCGATTGTCTGTGTGCGCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGCGAGAA 3218
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QY 5230 CATAAAACCGCCAGTCTAGCAACTGTGGGAAAGGCGATCGGTGCGGGCTCTTCGCTA 5289
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QY 5290 TTACGCCAGTGGCGAAAGGGGATGTGCTGCAAGCGGATTAAGTTGGGTAAAGCCAGGG 5349
Db 3459 TTACGCCAGTGGCGAAAGGGGATGTGCTGCAAGCGGATTAAGTTGGGTAAAGCCAGGG 3518
QY 5350 TTTTCCAGTCAGCAG 5365
Db 3519 TTTTCCAGTCAGCAG 3534
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RESULT 14

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US-10-395-709-15
; Sequence 15, Application US/10395709
; Publication No. US20040014645A1
; GENERAL INFORMATION:
; APPLICANT: Advivis
; TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL
; FILE REFERENCE: 108328.00115 - AVSI-0021P1
; CURRENT APPLICATION NUMBER: US/10/395,709
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the entire plasmid sequence for wildtype GHRH.
US-10-395-709-15
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Db 1359 GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTAGAGGTTAATTTGAGCTTGGCG 1418
QY 3250 TAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACACAAC 3309
Db 1419 TAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACACAAC 1478
QY 3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTAACTCACA 3369
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3159	DB	CCGATTGCTGTTGTGCCAGTCAATAGCCGAATAGCCTCTCCACCCCAAGCGCGCGAGAA	3218
5050	QY	CCTCGGTGCAATCAATCTTGTTCATCATGCGAAACGATCCTCATCTGTCTTGTATCA	5109
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GenCore version 5.1.7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	1773	32.7	2725	12	Sequence 23, Appl
4	1771.4	32.7	2700	12	Sequence 24, Appl
5	1771.4	32.7	2716	12	Sequence 33, Appl
6	1771.4	32.7	2716	12	Sequence 27, Appl
7	1771.4	32.7	2716	12	Sequence 28, Appl
8	1771.4	32.7	2716	12	Sequence 29, Appl
9	1771.4	32.7	2721	12	Sequence 31, Appl
10	1771.4	32.7	2721	12	Sequence 26, Appl
11	1771.4	32.7	2725	12	Sequence 34, Appl
12	1771.4	32.7	2725	12	Sequence 25, Appl
13	1771.4	32.7	2739	12	Sequence 32, Appl
14	1771.4	32.7	2739	12	Sequence 30, Appl
15	1372.8	25.3	2403	7	Sequence 1, Appl
16	1347.2	24.8	5181	12	Sequence 3, Appl
17	1347.2	24.8	5181	12	Sequence 19, Appl
18	1082.6	20.0	4968	12	Sequence 18, Appl
19	1082.6	20.0	5073	12	Sequence 8, Appl
20	1082.2	20.0	8953	12	Sequence 64, Appl

c 21	1081.2	19.9	5094	12	US-11-024-251-28	Sequence 28, Appl
c 22	1081.2	19.9	5103	12	US-11-024-251-26	Sequence 26, Appl
c 23	1081.2	19.9	5766	12	US-11-024-251-34	Sequence 34, Appl
c 24	1081.2	19.9	5972	12	US-11-024-251-30	Sequence 30, Appl
c 25	1081.2	19.9	6197	12	US-11-024-251-32	Sequence 32, Appl
c 26	1080.6	19.9	11110	7	US-10-978-927-20	Sequence 20, Appl
c 27	1080.6	19.9	12263	7	US-10-978-927-19	Sequence 19, Appl
c 28	1080	19.9	3448	12	US-11-024-959-773	Sequence 773, Appl
c 29	1080	19.9	5534	12	US-11-024-959-776	Sequence 776, Appl
c 30	1080	19.9	7160	12	US-11-024-959-777	Sequence 777, Appl
c 31	1079.4	19.9	5001	12	US-11-214-613-40	Sequence 40, Appl
c 32	1079.4	19.9	5034	12	US-11-214-613-33	Sequence 33, Appl
c 33	1079.4	19.9	5164	12	US-11-214-613-36	Sequence 36, Appl
c 34	1079.4	19.9	5277	12	US-11-214-613-25	Sequence 25, Appl
c 35	1079.4	19.9	5295	12	US-11-214-613-38	Sequence 38, Appl
c 36	1079.4	19.9	5327	12	US-11-214-613-27	Sequence 27, Appl
c 37	1079.4	19.9	5337	12	US-11-214-613-19	Sequence 19, Appl
c 38	1079.4	19.9	5337	12	US-11-214-613-23	Sequence 23, Appl
c 39	1079.4	19.9	5337	12	US-11-214-613-31	Sequence 31, Appl
c 40	1079.4	19.9	5338	12	US-11-214-613-15	Sequence 15, Appl
c 41	1079.4	19.9	5338	12	US-11-214-613-29	Sequence 29, Appl
c 42	1079.4	19.9	5345	12	US-11-214-613-17	Sequence 17, Appl
c 43	1079.4	19.9	5387	12	US-11-214-613-41	Sequence 41, Appl
c 44	1079.4	19.9	5395	12	US-11-214-613-21	Sequence 21, Appl
c 45	1079.4	19.9	7239	12	US-11-089-551A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1

US-11-186-282-22
; Sequence 22, Application US/11/186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Adviseys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 22
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid vector having an analog GHRH sequence.
US-11-186-282-22

Query Match	39.8%	Score 2160;	DB 12;	Length 3534;
Best Local Similarity	99.5%	Pred. No. 0;		
Matches 2166;	Conservative	0;	Mismatches 10;	Indels 0; Gaps 0;
QY	3190	GAGCCAGGGAACAAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTCCAGCTTGCGG	3249	
Db	1359	GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTCCAGCTTGCGG	1418	
QY	3250	TAATCATGTCATAGCTAGCTTTCTGTGTGAAATTTATTCGGCTCACAATTCACACAAC	3309	
Db	1419	TAATCATGTCATAGCTAGCTTTCTGTGTGAAATTTATTCGGCTCACAATTCACACAAC	1478	
QY	3310	ATACGAGCGGAGCATAAAGTCTAAAGCTGGGGTCCCTTAATGAGTGAGCTCACTCACA	3369	
Db	1479	ATACGAGCGGAGCATAAAGTCTAAAGCTGGGGTCCCTTAATGAGTGAGCTCACTCACA	1538	
QY	3370	TTAATTTGCGTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTCAGCTGCAT	3429	
Db	1539	TTAATTTGCGTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTCAGCTGCAT	1598	
QY	3430	TAATGAATCGGCCAACCGCGGGGAGCGGTTTCGGTATTGGGCGCTCTTCGGCTTCC	3489	
Db	1599	TAATGAATCGGCCAACCGCGGGGAGCGGTTTCGGTATTGGGCGCTCTTCGGCTTCC	1658	

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QY 3490 TCGCTCACTGACTGCTGCGCTCGCTTGGCTGCGGAGCGGTATCAGTCTCACTCA 3549
Db 1659 TCGCTCACTGACTGCTGCGCTCGCTTGGCTGCGGAGCGGTATCAGTCTCACTCA 1718
QY 3550 AAGCGGTAAATACGGTTATCCACAGATACAGGGATAAACAGCAAGAAACATGTGAGCA 3609
Db 1719 AAGCGGTAAATACGGTTATCCACAGATACAGGGATAAACAGCAAGAAACATGTGAGCA 1778
QY 3610 AAAGCCAGCAAAAGGCCAGCAACCGTAAAGGCCCGGTGCTGGCGTTTTCATAGG 3669
Db 1779 AAAGCCAGCAAAAGGCCAGCAACCGTAAAGGCCCGGTGCTGGCGTTTTCATAGG 1838
QY 3670 CTCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGCGCAAAACCCG 3729
Db 1839 CTCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGCGCAAAACCCG 1898
QY 3730 ACAGGACTATAAGATACCAAGGGTTTTCCCGCTGGAAAGCTCCCTCGTGCCTCTCTGTT 3789
Db 1899 ACAGGACTATAAGATACCAAGGGTTTTCCCGCTGGAAAGCTCCCTCGTGCCTCTCTGTT 1958
QY 3790 CCGACCTGCGGCTTACCGGATACCTGTCGCGCTTTCTCCGTTCCGGAAGGTGGCGCTT 3849
Db 1959 CCGACCTGCGGCTTACCGGATACCTGTCGCGCTTTCTCCGTTCCGGAAGGTGGCGCTT 2018
QY 3850 TCTCATAGCTCAGCTCTAGGTATCTCAGTTCGGGTAGTCTGTTCCGCTCCAGCTGGGC 3909
Db 2019 TCTCATAGCTCAGCTCTAGGTATCTCAGTTCGGGTAGTCTGTTCCGCTCCAGCTGGGC 2078
QY 3910 TGTGTGCAACAACCCCGCTTCAGCCGACCGCTGCGCCCTTATCCGGTAACTATCGTCTT 3969
Db 2079 TGTGTGCAACAACCCCGCTTCAGCCGACCGCTGCGCCCTTATCCGGTAACTATCGTCTT 2138
QY 3970 GAGTCCAAACCCGTAAGACACGACTTATCGCACTGCGAGCAGCACTGGTAACAGGATT 4029
Db 2139 GAGTCCAAACCCGTAAGACACGACTTATCGCACTGCGAGCAGCACTGGTAAACAGGATT 2198
QY 4030 AGCAGGCGGAGGTATGAGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTTACTAGGC 4089
Db 2199 AGCAGGCGGAGGTATGAGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTTACTAGGC 2258
QY 4090 TACACTAGAAAGAACAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGTACTCTTCGAAAA 4149
Db 2259 TACACTAGAAAGAACAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGTACTCTTCGAAAA 2318
QY 4150 AGAGTGGTAGCTCTTGATTCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGT 4209
Db 2319 AGAGTGGTAGCTCTTGATTCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGT 2378
QY 4210 TGCAGCAGCAGATTACGCGCAGAAAGAAAGGATCTCAAGAGATCCTTTGATCTTTTCT 4269
Db 2379 TGCAGCAGCAGATTACGCGCAGAAAGAAAGGATCTCAAGAGATCCTTTGATCTTTTCT 2438
QY 4270 ACGGGGCTGACGCTCAGAGAACTCGTCAAGAGGCGATAGAGGCGATGCGCTGCGAA 4329
Db 2439 ACGGGGCTGACGCTCAGAGAACTCGTCAAGAGGCGATAGAGGCGATGCGCTGCGAA 2498
QY 4330 TCGGAGCGCGCATACCGTAAAGCA CGAGGAAGCGGTACGCCCATTCGCCGCCAAGTCT 4389
Db 2499 TCGGAGCGCGCATACCGTAAAGCA CGAGGAAGCGGTACGCCCATTCGCCGCCAAGTCT 2558
QY 4390 TCAGCAATATACCGGTAGCCACGCTATGTCCTGATAGCGGTGCGGCACACCGCGG 4449
Db 2559 TCAGCAATATACCGGTAGCCACGCTATGTCCTGATAGCGGTGCGGCACACCGCGG 2618
QY 4450 CCACAGTCGATGAATCCAGAAAGCGGCATTTTCCACATGATATTCGCAACAGCA 4509
Db 2619 CCACAGTCGATGAATCCAGAAAGCGGCATTTTCCACATGATATTCGCAACAGCA 2678
QY 4510 TCGCCATGGGTACAGCAGAGATCTCTCGCGCTCGGCGATCGCGCTTGAGCTTCGCAAC 4569
Db 2679 TCGCCATGGGTACAGCAGAGATCTCTCGCGCTCGGCGATCGCGCTTGAGCTTCGCAAC 2738
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QY 4570 AGTTCCGCTGGCGGAGCCCTCGATGCTCTTCTGTCAGATCATCTCTGATCGAAGACCG 4629
Db 2739 AGTTCCGCTGGCGGAGCCCTCGATGCTCTTCTGTCAGATCATCTCTGATCGAAGACCG 2798
QY 4630 GCTTCATCCGAGTACGTGCTCGCTCGATCGATGTTTTCGTTGGTGGTGAATGGGCG 4689
Db 2799 GCTTCATCCGAGTACGTGCTCGCTCGATCGATGTTTTCGTTGGTGGTGAATGGGCG 2858
QY 4690 GTAGCCGGATCAAGCGTATGTCAGCCGCGCATTTGTCATCAGCCATGATGATCTTCTCG 4749
Db 2859 GTAGCCGGATCAAGCGTATGTCAGCCGCGCATTTGTCATCAGCCATGATGATCTTCTCG 2918
QY 4750 GCAGGAGCAAGGTGAGATGACAGAGATCTTGCCTCCGCGCATCTTGCCTCAATAGCAGCCAG 4809
Db 2919 GCAGGAGCAAGGTGAGATGACAGAGATCTTGCCTCCGCGCATCTTGCCTCAATAGCAGCCAG 2978
QY 4810 TCCCTTCCCGCTTCACTGACAAAGTCGAGCAGCAGTCGCGCAAGAAACCGCGTCTGGCC 4869
Db 2979 TCCCTTCCCGCTTCACTGACAAAGTCGAGCAGCAGTCGCGCAAGAAACCGCGTCTGGCC 3038
QY 4870 AGCCACGATAGCCGCTGCTCTGCTGAGTTCATTTCAGGGCACCGGACAGGTCCGTC 4929
Db 3039 AGCCACGATAGCCGCTGCTCTGCTGAGTTCATTTCAGGGCACCGGACAGGTCCGTC 3098
QY 4930 TTGACAAAAAGAACCCGGCGCCCTGCTGCTGACAGCCGCAACACGCGCGCATCAGAGCAG 4989
Db 3099 TTGACAAAAAGAACCCGGCGCCCTGCTGCTGACAGCCGCAACACGCGCGCATCAGAGCAG 3158
QY 4990 CCGATTGCTGTTGTGTCAGTCATAGCCGATAGCTCTTCCACCCAAAGCGCGCGAGAA 5049
Db 3159 CCGATTGCTGTTGTGTCAGTCATAGCCGATAGCTCTTCCACCCAAAGCGCGCGAGAA 3218
QY 5050 CTTGCGTGCATCCATCTTCTTCAATCATCGGAAACGATCCTCATCTCTCTTGTATCA 5109
Db 3219 CTTGCGTGCATCCATCTTCTTCAATCATCGGAAACGATCCTCATCTCTCTTGTATCA 3278
QY 5110 GATCTTGATCCCTTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
Db 3279 GATCTTGATCCCTTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3338
QY 5170 CAGGGCTTCCCAACCTTACAGAGGGCGCCCGCAGTGGCAATTCCGGTTTCGTTGCTGTC 5229
Db 3339 CAGGGCTTCCCAACCTTACAGAGGGCGCCCGCAGTGGCAATTCCGGTTTCGTTGCTGTC 3398
QY 5230 CATATAACCCCGCAGTCTAGCAACTGTTGGAGGGCGATCGGTGCGGGCTCTTTCGCTA 5289
Db 3399 CATATAACCCCGCAGTCTAGCAACTGTTGGAGGGCGATCGGTGCGGGCTCTTTCGCTA 3458
QY 5290 TTACGCCAGCTGGCGAAAGGGGATGTGCTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGG 5349
Db 3459 TTACGCCAGCTGGCGAAAGGGGATGTGCTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGG 3518
QY 5350 TTTTCCAGTCACGAC 5365
Db 3519 TTTTCCAGTCACGAC 3534
```

RESULT 2

US-11-186-282-23

; Sequence 23, Application US/11186282

; Publication No. US20060025368A1

; GENERAL INFORMATION:

; APPLICANT: Advisys, Inc.

; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response

; FILE REFERENCE: 108328.000265 AVSI-0042

; CURRENT APPLICATION NUMBER: US/11/186,282

; CURRENT FILING DATE: 2005-07-21

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 23

; LENGTH: 2722

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:									
; OTHER INFORMATION: Plasmid vector having a codon optimized mouse GHRH sequence									
US-11-186-282-23									
Query Match 32.78; Score 1773; DB 12; Length 2722;									
Best Local Similarity 98.6; Pred. No. 0;									
Matches 1803; Conservative 0; Mismatches 15; Indels 11; Gaps 1;									
QY	3454	AGAGGCGGTTGGGTATGAGCGCTCTTCGCGCTCTTCGCGTCTCACTGACTCGCTCGCGTCG	3513						
DB	860	AGTGAGGTTAAATTCGAGCTTGCTCTTCGCGTCTTCGCTCACTGACTCGCTCGCGTCG	919						
QY	3514	GTGCTTCGCGTTCGCGAGCGGTATCAGCTCACTCAAGGCGGTATATACGGTTATCCACA	3573						
DB	920	GTGCTTCGCGTTCGCGAGCGGTATCAGCTCACTCAAGGCGGTATATACGGTTATCCACA	979						
QY	3574	GAATCAGGGGATACCGAGGAAAGACATCTGACGAAAGGCGGCAAGAGGCGGAGAAC	3633						
DB	980	GAATCAGGGGATACCGAGGAAAGACATCTGACGAAAGGCGGCAAGAGGCGGAGAAC	1039						
QY	3634	CGTAAAGGCGCGTTCGCGGCTTTTCCATAGGCTCCGCCCTCGAGCATCAC	3693						
DB	1040	CGTAAAGGCGCGTTCGCGGCTTTTCCATAGGCTCCGCCCTCGAGCATCAC	1099						
QY	3694	AAAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATATAAGATACAGGCG	3753						
DB	1100	AAAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATATAAGATACAGGCG	1159						
QY	3754	TTTCCCGCTCGAAGCTCCCTCGCGCTCTTCGCGTTCGCGACCTCGCGCTTACCGGATAC	3813						
DB	1160	TTTCCCGCTCGAAGCTCCCTCGCGCTCTTCGCGTTCGCGACCTCGCGCTTACCGGATAC	1219						
QY	3814	CTGTCCGCTCTTCGCGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	3873						
DB	1220	CTGTCCGCTCTTCGCGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	1279						
QY	3874	CTCAGTTCGCTGAGTTCGCTCAAGCTGGCTGTGTGCAAGAACCCCGCTTCAG	3933						
DB	1280	CTCAGTTCGCTGAGTTCGCTCAAGCTGGCTGTGTGCAAGAACCCCGCTTCAG	1339						
QY	3934	CCGACCGCTCGGCTTATCCGCTTACTATCTGCTTGGTTCGACCCGCTAAGACGAC	3993						
DB	1340	CCGACCGCTCGGCTTATCCGCTTACTATCTGCTTGGTTCGACCCGCTAAGACGAC	1399						
QY	3994	TTATCGGCTCGGACGAGCACTGGTAAACAGGATAGCAGAGCGAGGTATGTAGCGGT	4053						
DB	1400	TTATCGGCTCGGACGAGCACTGGTAAACAGGATAGCAGAGCGAGGTATGTAGCGGT	1459						
QY	4054	GCTACAGAGTTCGAGTTCGCTTAACTACGCTTACACTAGAGAAACAGTATTGGT	4113						
DB	1460	GCTACAGAGTTCGAGTTCGCTTAACTACGCTTACACTAGAGAAACAGTATTGGT	1519						
QY	4114	ATCTGCGCTCTGTAAGCCAGTTACTCTCGGAAAGAGTTGGTAGCTCTTCAATCGGC	4173						
DB	1520	ATCTGCGCTCTGTAAGCCAGTTACTCTCGGAAAGAGTTGGTAGCTCTTCAATCGGC	1579						
QY	4174	AAACAAACACCGCTGAGCGGTGTTTTTTTGTGTAAGCAGCAGATTTAGCGCAGA	4233						
DB	1580	AAACAAACACCGCTGAGCGGTGTTTTTTTGTGTAAGCAGCAGATTTAGCGCAGA	1639						
QY	4234	AAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGCGGCTCTGA	4282						
DB	1640	AAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGCGGCTCTGA	1699						
QY	4283	CTCAGAAGACTCGTCAAGAGGCGATAGAGGCGATGCGCTCGGAATCGGGAGCGCGCA	4342						
DB	1700	CTCAGAAGACTCGTCAAGAGGCGATAGAGGCGATGCGCTCGGAATCGGGAGCGCGCA	1759						
QY	4343	TACCGTAAAGCAGGAGGAGCGGTACGCCATTCGCGCGCAAGCTCTTCAGCAATATCAC	4402						
DB	1760	TACCGTAAAGCAGGAGGAGCGGTACGCCATTCGCGCGCAAGCTCTTCAGCAATATCAC	1819						
QY	4403	GGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCGCACACCCAGCGCGGCCACAGTCGATGA	4462						

RESULT 3
US-11-186-282-24
; Sequence 282, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24

```
; LENGTH: 2725
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid vector having a codon optimized rat GHRH sequence
US-11-186-282-24

Query Match      32.78; Score 1773; DB 12; Length 2725;
Best Local Similarity 98.68; Pred. No. 0;
Matches 1803; Conservative 0; Mismatches 15; Indels 11; Gaps 1;

Qy 3454 AGAGCGGCTTGGCGTATTGGCGCTCTTCGGCTCTCTCGCTCACTGACTCGCTCGCTCG 3513
Db      |||
Qy 863 AGTGAGGTTAAATTCGAGCTTGGCTCTTCGGCTCTCTCGCTCACTGACTCGCTCGCTCG 922
Db      |||
Qy 3514 GTCTTCGGCTGCGCGAGCGGTATACAGCTCACTCAAAGGGGTTAATACGGTTATCCACA 3573
Db      |||
Qy 923 GTCTTCGGCTGCGCGAGCGGTATACAGCTCACTCAAAGGCGGTTAATACGGTTATCCACA 982
Db      |||
Qy 3574 GAATCAGGGGATACGAGGAAAGAACATGTGACAAAGGCGGCAAGGCGGAGGCGGAGAAC 3633
Db      |||
Qy 983 GAATCAGGGGATACGAGGAAAGAACATGTGAGAAAGGCGGCAAGGCGGAGGCGGAGAAC 1042
Db      |||
Qy 3634 CGTAAAGGCGCGTGTGCTGGCGCTTTTTCATAGGCTCCGCCCCCTGACGAGCATCAC 3693
Db      |||
Qy 1043 CGTAAAGGCGCGTGTGCTGGCGCTTTTTCATAGGCTCCGCCCCCTGACGAGCATCAC 1102
Db      |||
Qy 3694 AAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCG 3753
Db      |||
Qy 1103 AAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCG 1162
Db      |||
Qy 3754 TTTCCCGCTGGAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC 3813
Db      |||
Qy 1163 TTTCCCGCTGGAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC 1222
Db      |||
Qy 3814 CTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTAT 3873
Db      |||
Qy 1223 CTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTAT 1282
Db      |||
Qy 3874 CTCAAGTCGGGTAGGTGCTTGGCTCAAGCTGGGTGTGTGCAAGAACCCCGCTTCAG 3933
Db      |||
Qy 1283 CTCAAGTCGGGTAGGTGCTTGGCTCAAGCTGGGTGTGTGCAAGAACCCCGCTTCAG 1342
Db      |||
Qy 3934 CCCAGCGCTGCGCTTATCGGTAACTATGCTTCAGTCCACCCGCTAAGACAGAC 3993
Db      |||
Qy 1343 CCCAGCGCTGCGCTTATCGGTAACTATGCTTCAGTCCACCCGCTAAGACAGAC 1402
Db      |||
Qy 3994 TTATCGGCACCTGGCAGCAGCACCTGGTAAACAGGATTAAGCAGAGCGAGGTATGTAGGCGGT 4053
Db      |||
Qy 1403 TTATCGGCACCTGGCAGCAGCACCTGGTAAACAGGATTAAGCAGAGCGAGGTATGTAGGCGGT 1462
Db      |||
Qy 4054 GCTACAGAGTCTTGAAAGTGGTGGCTTAACTACGGCTACACTAGAAGAACAGTATTTGGT 4113
Db      |||
Qy 1463 GCTACAGAGTCTTGAAAGTGGTGGCTTAACTACGGCTACACTAGAAGAACAGTATTTGGT 1522
Db      |||
Qy 4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGTAGCTCTTGATCCGGC 4173
Db      |||
Qy 1523 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGTAGCTCTTGATCCGGC 1582
Db      |||
Qy 4174 AAACAAACCCAGCTGGTAGCGGTGGTTTTTTTGTGTAAGCAGCAGAGTTACCGCGAGA 4233
Db      |||
Qy 1583 AAACAAACCCAGCTGGTAGCGGTGGTTTTTTTGTGTAAGCAGCAGAGTTACCGCGAGA 1642
Db      |||
Qy 4234 AAAAAAGATCTCAAGAGATCTTTGATCTTTTCTACGGGCTCTGA-----CG 4282
Db      |||
Qy 1643 AAAAAAGATCTCAAGAGATCTTTGATCTTTTCTACGGGCTCTGACGCTCAGCTAGCG 1702
Db      |||
Qy 4283 CTCAAGAGATCTCTCAAGAGCGATAGAGGCGATCGCTCGAATCGGAGCGGCGGA 4342
Db      |||
Qy 1703 CTCAAGAGATCTCTCAAGAGCGGATAGAGGCGATCGCTCGAATCGGAGCGGCGGA 1762
Db      |||
Qy 4343 TACCGTAAAGCAGCAGGAGGCGGTACGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAC 4402
Db      |||
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Db 1763 TACCGTAAAGCAGCAGGAGGCGGTACGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAC 1822
Qy 4403 GGGTAGCCAAACGCTATGTCTGATAGCGGTCCGCCACACCCAGCCGSCACAGTCCGATGA 4462
Db 1823 GGGTAGCCAAACGCTATGTCTGATAGCGGTCCGCCACACCCAGCCGSCACAGTCCGATGA 1882
Qy 4463 ATCCAGAAAGCGCGCATTTTTCACCATGATATTCGCGCAAGCAGGATCCGCCATGGGTCA 4522
Db 1883 ATCCAGAAAGCGCGCATTTTTCACCATGATATTCGCGCAAGCAGGATCCGCCATGGGTCA 1942
Qy 4523 CGACGAGATCTCTCGCGTGGCGCATGCGCGCTTGAGCTCTGGCGAAACAGTTCGGCTGGCG 4582
Db 1943 CGACGAGATCTCTCGCGTGGCGCATGCGCGCTTGAGCTCTGGCGAAACAGTTCGGCTGGCG 2002
Qy 4583 CGAGCCCTGATGCTCTTGGTCCAGATCATCTCTGATCGACCAAGCCGGCTTCATCCGAG 4642
Db 2003 CGAGCCCTGATGCTCTTGGTCCAGATCATCTCTGATCGACCAAGCCGGCTTCATCCGAG 2062
Qy 4643 TAGCTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGGATCAA 4702
Db 2063 TAGCTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGGATCAA 2122
Qy 4703 GCGTATGACGCCCGCCCATTTGCATCAGCCATGATGATACTTCTCGGCAAGGCAAGGT 4762
Db 2123 GCGTATGACGCCCGCCCATTTGCATCAGCCATGATGATACTTCTCGGCAAGGCAAGGT 2182
Qy 4763 GAGATGACAGGAGATCTTGGCCCGGCACTTTCGCGCAATAGCAGCCAGTCCCTTCGCGTT 4822
Db 2183 GAGATGACAGGAGATCTTGGCCCGGCACTTTCGCGCAATAGCAGCCAGTCCCTTCGCGTT 2242
Qy 4823 CAGTGACAAAGCTGCGACAGCTGCGCAAGAAACGCGCTGCTGGCGCAGCAGCATAGGCC 4882
Db 2243 CAGTGACAAAGCTGCGACAGCTGCGCAAGAAACGCGCTGCTGGCGCAGCAGCATAGGCC 2302
Qy 4883 GCGCTGCTGCTCCTCGAGTTCAATTAGGGCACCGGACAGGTTCGGTCTTGACAAAAGAA 4942
Db 2303 GCGCTGCTGCTCCTCGAGTTCAATTAGGGCACCGGACAGGTTCGGTCTTGACAAAAGAA 2362
Qy 4943 CCGGGCGCCCTGCGCTGACGCGGNAACAGGGGCGCATCAGAGCAGCCGATGCTGTT 5002
Db 2363 CCGGGCGCCCTGCGCTGACGCGGNAACAGGGGCGCATCAGAGCAGCCGATGCTGTT 2422
Qy 5003 GTGCCAGATCATAGCCGAATAGCTCTCCACCAAGCGCGCGAGAACCTTCGCTGCAATC 5062
Db 2423 GTGCCAGATCATAGCCGAATAGCTCTCCACCAAGCGCGCGAGAACCTTCGCTGCAATC 2482
Qy 5063 CATCTTTGTTCAATCATGCGAAACGATCTCATCTGCTCTTGTATCAGATCTTGATCCCC 5122
Db 2483 CATCTTTGTTCAATCATGCGAAACGATCTCATCTGCTCTTGTATCAGATCTTGATCCCC 2542
Qy 5123 TGGCGCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCCAA 5182
Db 2543 TGGCGCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCCAA 2602
Qy 5183 CTTTACAGAGGCGCGCCAGCTGGCAATTCGCGTTCGCTTGTCTCATATAAACCGCCCC 5242
Db 2603 CTTTACAGAGGCGCGCCAGCTGGCAATTCGCGTTCGCTTGTCTCATATAAACCGCCCC 2662
Qy 5243 AGTCTAGCAACTGTGCGGAAGGCGGATCG 5271
Db 2663 AGTCTAGCAACTGTGCGGAAGGCGGATCG 2691
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RESULT 4
US-11-186-282-33
; Sequence 33, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21


```

; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized dog-CHRH expression plasmid.
US-11-186-282-27

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Query Match	32.7%	Score 1771.4	DB 12	Length 2716
Best Local Similarity	98.5%	Pred. No. 0		
Matches 1802	Conservative 0	Mismatches 16	Indels 11	Gaps 1
Qy	3454	AGAGGCGTTTGCGTATTGGCGCTCTTCGCGTTCCTCGCTTCAGTGA	CTCGCTCGCTGCGTCTCG	3513
Db	854	AGTGAGGTTAAATTTTCAGCTTGCTTCGCGTTCCTCGCTTCAGTGA	CTCGCTCGCTGCGTCTCG	913
Qy	3514	GTCGTTTCGCGTCGCGCAGCGGTATCAGCTCACTCAAAGCGGTAATACGGT	TATCCACA	3573
Db	914	GTCGTTTCGCGTCGCGCAGCGGTATCAGCTCACTCAAAGCGGTAATACGGT	TATCCACA	973
Qy	3574	GAATCAGGGGATTAACGACAGAAAGAAATGTGAGCAAAAGCCAGCAAAAGCCAGGAAC		3633
Db	974	GAATCAGGGGATTAACGACAGAAAGAAATGTGAGCAAAAGCCAGCAAAAGCCAGGAAC		1033
Qy	3634	CGTAAAGCGCGTTGCTGGCGTTCCTATAGGCTTCGCCCCCTGACGAGCATCAC		3693
Db	1034	CGTAAAGCGCGTTGCTGGCGTTCCTATAGGCTTCGCCCCCTGACGAGCATCAC		1093
Qy	3694	AAAATCGACGCTCAAAGTCAGAGTGCAGAAACCCGACAGACTATAAAGATACCAAGCGC		3753
Db	1094	AAAATCGACGCTCAAAGTCAGAGTGCAGAAACCCGACAGACTATAAAGATACCAAGCGC		1153
Qy	3754	TTTTCCCTCGAAGCTCCTCGTGCCTCTCTGTTCGACCCCTGCGCTTACCGGATAC		3813
Db	1154	TTTTCCCTCGAAGCTCCTCGTGCCTCTCTGTTCGACCCCTGCGCTTACCGGATAC		1213
Qy	3814	CTGTCGCGCTTTCTCCCTTCGGGAAGGTGGCGCTTCTCATAGCTCACCGTGTAGTAT		3873
Db	1214	CTGTCGCGCTTTCTCCCTTCGGGAAGGTGGCGCTTCTCATAGCTCACCGTGTAGTAT		1273
Qy	3874	CTCAGTTCCGGTGTAGTGCCTTCGCTCCAAAGCTGGGCTGTGACAGAACCCCGCTTCAG		3933
Db	1274	CTCAGTTCCGGTGTAGTGCCTTCGCTCCAAAGCTGGGCTGTGACAGAACCCCGCTTCAG		1333
Qy	3934	CCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAGACACGAC		3993
Db	1334	CCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAGACACGAC		1393
Qy	3994	TTATCGCACTGGCAGCAGCACTGGTAAACAGGATTAAGCAGCGAGGTATGAGCGCGT		4053
Db	1394	TTATCGCACTGGCAGCAGCACTGGTAAACAGGATTAAGCAGCGAGGTATGAGCGCGT		1453
Qy	4054	GCTACAGAGTCTTGAAGTGGTGCCTTAACTACGGCTACACTAGAAAGACAGTATTTGGT		4113
Db	1454	GCTACAGAGTCTTGAAGTGGTGCCTTAACTACGGCTACACTAGAAAGACAGTATTTGGT		1513
Qy	4114	ATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGAAAAAAGAGTTGGTAGCTCTTTGATCCGGC		4173
Db	1514	ATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGAAAAAAGAGTTGGTAGCTCTTTGATCCGGC		1573
Qy	4174	AAACAAACCAACCGCTGGTAGCGGTGTTTTTTTGTTCGACGACGACAGATTACCGCAGGA		4233
Db	1574	AAACAAACCAACCGCTGGTAGCGGTGTTTTTTTGTTCGACGACGACAGATTACCGCAGGA		1633
Qy	4234	AAAAAGGATCTAAGAAAGATCCTTTGATCTTTTCTAGCGGGTCTGTA-----CG		4282
Db	1634	AAAAAGGATCTAAGAAAGATCCTTTGATCTTTTCTAGCGGGTCTGACGCTCAGTACGCG		1693

RESULT 6
US-11-186-282-28
; sequence 28, Application US/11186282
; Publication No. US20060025368A1

GENERAL INFORMATION:
; APPLICANT: Advists, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized bovine-GHRH expression plasmid.
US-11-186-282-28

Query Match		32.7%;	Score 1771.4;	DB 12;	Length 2716;
Best Local Similarity		98.5%;	Pred. No. 0;		
Matches 1802; Conservative		0;	Mismatches 16;	Indels 11;	Gaps 1;
QY	3454	AGAGGCGGTTTGGGCTATTGGGCGCTCTTTCGCTTTCCTCGCTCACTGACTGCTCGCTCGCTCG	3513		
DB	854	AGTAGGGTTAATTCGAGCTTGGTCTTCGCTTCTCGCTCACTGACTGCTCGCTCGCTCG	913		
QY	3514	GTGCTTCGGTCGCGGAGCGGTATCAGCTCACTCAAGAGCGGTAAATACGGTTATCCACA	3573		
DB	914	GTGCTTCGGTCGCGGAGCGGTATCAGCTCACTCAAGAGCGGTAAATACGGTTATCCACA	973		
QY	3574	GAATCAGGGGATAACCGCAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC	3633		
DB	974	GAATCAGGGGATAACCGCAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC	1033		
QY	3634	CGTAAAAAGCCCGCTTGTCTGGCGTTTTCATAGGCTCGCGCCCTCGACGAGCATCAC	3693		
DB	1034	CGTAAAAAGCCCGCTTGTCTGGCGTTTTCATAGGCTCGCGCCCTCGACGAGCATCAC	1093		
QY	3694	AAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCGACAGGACTATAAAGATACCAAGCG	3753		
DB	1094	AAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCGACAGGACTATAAAGATACCAAGCG	1153		
QY	3754	TTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC	3813		
DB	1154	TTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC	1213		
QY	3814	CTGTCCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTAT	3873		
DB	1214	CTGTCCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTAT	1273		
QY	3874	CTCAGTTCGCTGTAGTCTGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAG	3933		
DB	1274	CTCAGTTCGCTGTAGTCTGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAG	1333		
QY	3934	CCGACCGCTCGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTTAAGACAGCAC	3993		
DB	1334	CCGACCGCTCGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTTAAGACAGCAC	1393		
QY	3994	TTATCGCACTGCGCAGCAGCACTGGTAAACAGATTAGCAGAGGAGGTATGTAGCGGT	4053		
DB	1394	TTATCGCACTGCGCAGCAGCACTGGTAAACAGATTAGCAGAGGAGGTATGTAGCGGT	1453		
QY	4054	GCTACAGAGTTCTTGAAGTGGTGGCCCTAACCTACGGCTACACTAGAGAAACAGATTATTGGT	4113		
DB	1454	GCTACAGAGTTCTTGAAGTGGTGGCCCTAACCTACGGCTACACTAGAGAAACAGATTATTGGT	1513		
QY	4114	ATCTGGCTCTGCTGAAGCAGGTATACCTTCGGAAGAAAGAGTTGGTAGCTCTTGATCCGGC	4173		
DB	1514	ATCTGGCTCTGCTGAAGCAGGTATACCTTCGGAAGAAAGAGTTGGTAGCTCTTGATCCGGC	1573		
QY	4174	AAAAAACACCGCTGCTAGCGGTGGTTTTTTTGGTGGTAAAGCAGACAGATTACCGCGAGA	4233		
DB	1574	AAAAAACACCGCTGCTAGCGGTGGTTTTTTTGGTGGTAAAGCAGACAGATTACCGCGAGA	1633		
QY	4234	AAAAAAGGATCTCAAGAGATCCTTTTGTATCTTTTCTACGGGGTCTGA-----CG	4282		

RESULT 7

DB	1634	AAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG	1693
QY	4283	CTCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTCGGAATCGGAGCGCGGA	4342
DB	1694	CTCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTCGGAATCGGAGCGCGGA	1753
QY	4343	TACCGTAAAGACAGAGAAAGCGGTAGCCCATTTGCGCGCAAGCTCTTTACGCAATATCAC	4402
DB	1754	TACCGTAAAGACAGAGAAAGCGGTAGCCCATTTGCGCGCAAGCTCTTTACGCAATATCAC	1813
QY	4403	GGGTAGCCAAACGCTATGTCCTGATAGCGGTTCGCGCACACCCAGCGCGGCACAGTCCGATGA	4462
DB	1814	GGGTAGCCAAACGCTATGTCCTGATAGCGGTTCGCGCACACCCAGCGCGGCACAGTCCGATGA	1873
QY	4463	ATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGATCCGCCATGGGTCA	4522
DB	1874	ATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGATCCGCCATGGGTCA	1933
QY	4523	CGACGAGATCCTCGCGTCGCGCATGCGCGCTTTGAGCCTTGGCGAAACAGTTCCGCTGGCG	4582
DB	1934	CGACGAGATCCTCGCGTCGCGCATGCGCGCTTTGAGCCTTGGCGAAACAGTTCCGCTGGCG	1993
QY	4583	CGAGCCCCGTGATGCTCTTCCGTCCAGATCATCTGTGATCGACAGACCGGCTTCCATCCGAG	4642
DB	1994	CGAGCCCCGTGATGCTCTTCCGTCCAGATCATCTGTGATCGACAGACCGGCTTCCATCCGAG	2053
QY	4643	TACGCTCTCGCTCGATGCGATGTTTCGCTTGGTGGTCCGATGGCAGGTAGCCGATCAAA	4702
DB	2054	TACGCTCTCGCTCGATGCGATGTTTCGCTTGGTGGTCCGATGGCAGGTAGCCGATCAAA	2113
QY	4703	GGGTATGACAGCCCGCATTTGCATCAGCCATGATGGATACTTTCTCGGCAGGACAGGT	4762
DB	2114	GGGTATGACAGCCCGCATTTGCATCAGCCATGATGGATACTTTCTCGGCAGGACAGGT	2173
QY	4763	GAGATGACAGGAGATCCTGCGCCCGGCACTTTCGCGCAATAGCAGCCAGTCCCTTCCCGCTT	4822
DB	2174	GAGATGACAGGAGATCCTGCGCCCGGCACTTTCGCGCAATAGCAGCCAGTCCCTTCCCGCTT	2233
QY	4823	CAGTGACAAAGTGCAGCACAGCTGCGCAAGGAAACCGCTGCGGCGCAGCACGATAGCC	4882
DB	2234	CAGTGACAAAGTGCAGCACAGCTGCGCAAGGAAACCGCTGCGGCGCAGCACGATAGCC	2293
QY	4883	GGCTGCTCTGCTGTCAGTTTCAATTCAGGGCACCGGACAGGTCTGTTGACAAAAAGAA	4942
DB	2294	GGCTGCTCTGCTGTCAGTTTCAATTCAGGGCACCGGACAGGTCTGTTGACAAAAAGAA	2353
QY	4943	CGGGCGCCCTGCGCTGACAGCCGGAAACACCGCGCGCATCAGACGACCGATTTGCTGTT	5002
DB	2354	CGGGCGCCCTGCGCTGACAGCCGGAAACACCGCGCGCATCAGACGACCGATTTGCTGTT	2413
QY	5003	GTGCCAGTCAATGCGGAAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGCATC	5062
DB	2414	GTGCCAGTCAATGCGGAAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGCATC	2473
QY	5063	CATCTTGTTCATATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	5122
DB	2474	CATCTTGTTCATATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2533
QY	5123	TGCGCATCAGATCTTGGCGGCAAGAAAGCAATCCAGTTTACTTTGAGGGCTTCCCAA	5182
DB	2534	TGCGCATCAGATCTTGGCGGCAAGAAAGCAATCCAGTTTACTTTGAGGGCTTCCCAA	2593
QY	5183	CCTTACAGAGGGCGCCCGCAGCTGGCAATTTCCGGTTCCGTTGCTGCTCCATAAAACCGCCC	5242
DB	2594	CCTTACAGAGGGCGCCCGCAGCTGGCAATTTCCGGTTCCGTTGCTGCTCCATAAAACCGCCC	2653
QY	5243	AGTCTAGCAACTGTTGGGAAAGGCGGATCG	5271
DB	2654	AGTCTAGCAACTGTTGGGAAAGGCGGATCG	2682

US-11-186-282-29
; Sequence 29, Application US/11186282
; Publication No. US20060025369A1
; GENERAL INFORMATION:
; APPLICANT: Advivia, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328, 000265, AVS1-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized cat-GHRH expression plasmid.
US-11-186-282-29

Query Match 32.7%; Score 1771.4; DB 12; Length 2716;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

QY	3454	AGAGGCGGTTTGGCTATTGGCGCTCTTCCGCTTCCCTCGCTCACTGACTCGCTGCGCTCG	3513
DB	854	AGTGAGGGTTAAATTCAGACTTGGTCTTCGCTTCCCTCGCTCACTGACTCGCTGCGCTCG	913
QY	3514	GTGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAAGCGGGTAATACGGTTATCCACA	3573
DB	914	GTGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAAGCGGGTAATACGGTTATCCACA	973
QY	3574	GAATCAGGGGATAACGAGGAAGAACATGTGAGCAAAAGCCGACGAAAGGCCGAGCAAC	3633
DB	974	GAATCAGGGGATAACGAGGAAGAACATGTGAGCAAAAGCCGACGAAAGGCCGAGCAAC	1033
QY	3634	CGTAAAGAGCGCGTGTGGCGCTTTTCCATAGGCTCCGCCCCCTTGACGAGCATCAC	3693
DB	1034	CGTAAAGAGCGCGTGTGGCGCTTTTCCATAGGCTCCGCCCCCTTGACGAGCATCAC	1093
QY	3694	AAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGSACTATAAAGATACCAAGCG	3753
DB	1094	AAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGSACTATAAAGATACCAAGCG	1153
QY	3754	TTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTTCGCGCTTACCGGATAC	3813
DB	1154	TTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTTCGCGCTTACCGGATAC	1213
QY	3814	CTGTCCGCTTTCTCCCTTCGGGAAGGCTGGCGCTTTCTCATAGCTCAAGCTGTAGGTAT	3873
DB	1214	CTGTCCGCTTTCTCCCTTCGGGAAGGCTGGCGCTTTCTCATAGCTCAAGCTGTAGGTAT	1273
QY	3874	CTCAGTTCCGTTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGTTCCAG	3933
DB	1274	CTCAGTTCCGTTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGTTCCAG	1333
QY	3934	CCGACCGCTCGGCTTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGTTAAGACGAC	3993
DB	1334	CCGACCGCTCGGCTTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGTTAAGACGAC	1393
QY	3994	TTATCGCCACTGGCAGCAGCCACTTGGTAAACAGGATTTAGCAGCGAGGTATGTAGGCGGT	4053
DB	1394	TTATCGCCACTGGCAGCAGCCACTTGGTAAACAGGATTTAGCAGCGAGGTATGTAGGCGGT	1453
QY	4054	GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACCGGCTACATAGAGAACAGTATTTGGT	4113
DB	1454	GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACCGGCTACATAGAGAACAGTATTTGGT	1513
QY	4114	ATCTCGGCTCTGTGAAGCCAGTTACCTTCGAAAGAGTGTGTAGTCTTTGATCCGGC	4173
DB	1514	ATCTCGGCTCTGTGAAGCCAGTTACCTTCGAAAGAGTGTGTAGTCTTTGATCCGGC	1573
QY	4174	AAACAAACCCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTACGCGAGA	4233

DB	1574	AAACAAACCCGCTGGTAGCGGTGTTTTTTTTTTTAAAGCAGCAGATTACGCGAGA	1633
QY	4234	AAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGGTCTGA-----CG	4282
DB	1634	AAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGGTCTGA-----CG	1693
QY	4283	CTCAGAAGAACTCGTCAAGAAGCGGATAGAAAGCGATGCGCTGCGAATCGGGAGCGCGA	4342
DB	1694	CTCAGAAGAACTCGTCAAGAAGCGGATAGAAAGCGATGCGCTGCGAATCGGGAGCGCGA	1753
QY	4343	TACCGTAAAGCACGAGGAAGCGGTAGCCCATTCGCGCGCAAGCTCTTCAAGCAATATCAC	4402
DB	1754	TACCGTAAAGCACGAGGAAGCGGTAGCCCATTCGCGCGCAAGCTCTTCAAGCAATATCAC	1813
QY	4403	GGGTAGCCAAAGCTATGTCTGATAGCGGTCCGCCACACCCAGCGCGCACAGTCGATGA	4462
DB	1814	GGGTAGCCAAAGCTATGTCTGATAGCGGTCCGCCACACCCAGCGCGCACAGTCGATGA	1873
QY	4463	ATCCAGAAAGCGGCCAATTTTCCACATGATATTCCGCAAGCAGGCAATCGCCATGGGTCA	4522
DB	1874	ATCCAGAAAGCGGCCAATTTTCCACATGATATTCCGCAAGCAGGCAATCGCCATGGGTCA	1933
QY	4523	CGACAGATCCTCGCGTGGGCAATGCGCGCTTGAGCCTTGGGCAACAGTTTGGCTGGCG	4582
DB	1934	CGACAGATCCTCGCGTGGGCAATGCGCGCTTGAGCCTTGGGCAACAGTTTGGCTGGCG	1993
QY	4583	CGAGCCCTGATGCTCTTCGTCAGATCATCTTGATCGAACAGCCGGCTTCCATCCGAG	4642
DB	1994	CGAGCCCTGATGCTCTTCGTCAGATCATCTTGATCGAACAGCCGGCTTCCATCCGAG	2053
QY	4643	TACGTGCTCGCTCGATGCGATGTTTCGTTTGGTGGTGGATGGCAGGTAGCCGGATCAA	4702
DB	2054	TACGTGCTCGCTCGATGCGATGTTTCGTTTGGTGGTGGATGGCAGGTAGCCGGATCAA	2113
QY	4703	GCGTATGACGCGCGCATTTGCATCAGCCATGATGGATATCTTCTCGGCAAGCAAGGT	4762
DB	2114	GCGTATGACGCGCGCATTTGCATCAGCCATGATGGATATCTTCTCGGCAAGCAAGGT	2173
QY	4763	GAGTGAACAGGATCTGCGCCCGGACATTCGCGCCATAGCAGCAGTCCCTTCCCGCTT	4822
DB	2174	GAGTGAACAGGATCTGCGCCCGGACATTCGCGCCATAGCAGCAGTCCCTTCCCGCTT	2233
QY	4823	CAGTGACAAAGTTCAGACACAGCTGCGCAAGCAAGCCCGCTGTCGCCAGCCACGATAGCC	4882
DB	2234	CAGTGACAAAGTTCAGACACAGCTGCGCAAGCAAGCCCGCTGTCGCCAGCCACGATAGCC	2293
QY	4883	GCGCTGCTCGTCTGCTGAGTTCAATTCAGGGCAACGAGTCGCTTGTGCAAAAAGAA	4942
DB	2294	GCGCTGCTCGTCTGCTGAGTTCAATTCAGGGCAACGAGTCGCTTGTGCAAAAAGAA	2353
QY	4943	CGGGCGCCCTGCGCTGACAGCGGAACAGCGGGCATCAGAGCAGCGATTCGTCTGTT	5002
DB	2354	CGGGCGCCCTGCGCTGACAGCGGAACAGCGGGCATCAGAGCAGCGATTCGTCTGTT	2413
QY	5003	GTGCCAGTCAATAGCCGAATAGCCTCTCCACCCAGCGCGCGAGAACTCTCGTGCATC	5062
DB	2414	GTGCCAGTCAATAGCCGAATAGCCTCTCCACCCAGCGCGCGAGAACTCTCGTGCATC	2473
QY	5063	CATCTGTTTCAATCATCGGAAACGATCCTCATCTGCTCTTTGATCAGATCTTGATCCCC	5122
DB	2474	CATCTGTTTCAATCATCGGAAACGATCCTCATCTGCTCTTTGATCAGATCTTGATCCCC	2533
QY	5123	TGCGCCATCAGATCTTTGGCGGAAGAAAGCCATCCAGTTTACCTTCAGGGCTTCCCAA	5182
DB	2534	TGCGCCATCAGATCTTTGGCGGAAGAAAGCCATCCAGTTTACCTTCAGGGCTTCCCAA	2593
QY	5183	CTTTACAGAGGGCGCCCGAGCTGGCAATTCGCGTTGGCTTGTCTCATAAAAACCGCCC	5242
DB	2594	CTTTACAGAGGGCGCCCGAGCTGGCAATTCGCGTTGGCTTGTCTCATAAAAACCGCCC	2653
QY	5243	AGTCTAGCAACTGTGTGGAAAGGGCGATCG	5271
DB	2654	AGTCTAGCAACTGTGTGGAAAGGGCGATCG	2682

RESULT 8
US-11-186-282-31
; Sequence 31, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advists, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized ovine-GHRH expression plasmid.
US-11-186-282-31

Query Match 32.7%; Score 1771.4; DB 12; Length 2716;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

QY 3454 AGAGGCGGTTTGGGTATFTGGCGCTCTTCGCGCTTCTCGCTCACTCACTCGCTCGCTCG 3513
DB 854 AGTGAGGGTTAATTTTCGAGCTTGGTCTTCGCTTCTCGCTCACTCACTCGCTCGCTCG 913

QY 3514 GTCGTTGCGTGGCGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCACA 3573
DB 914 GTCGTTGCGTGGCGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCACA 973

QY 3574 GAATCAGGGATACCGAGGAAGACATGTGACCAAGGCCAGCAAGGCCAGGAAC 3633
DB 974 GAATCAGGGATACCGAGGAAGACATGTGACCAAGGCCAGCAAGGCCAGGAAC 1033

QY 3634 CGTAAAGGCGCGTGTGCGGTTTTTCATAGGCTCGCGCCCTCGACAGCATCAC 3693
DB 1034 CGTAAAGGCGCGTGTGCGGTTTTTCATAGGCTCGCGCCCTCGACAGCATCAC 1093

QY 3694 AAAAAATGACGCTCAAGTACAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGCG 3753
DB 1094 AAAAAATGACGCTCAAGTACAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGCG 1153

QY 3754 TTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC 3813
DB 1154 TTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC 1213

QY 3814 CTGTCGCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGAGGTAT 3873
DB 1214 CTGTCGCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGAGGTAT 1273

QY 3874 CTGAGTTGCGTGTAGTTCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAG 3933
DB 1274 CTGAGTTGCGTGTAGTTCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAG 1333

QY 3934 CCGAGCGCTGCGCTTATCCGCTTAATCTGTTAGTCCAAACCCGCTTAAGACAGAC 3993
DB 1334 CCGAGCGCTGCGCTTATCCGCTTAATCTGTTAGTCCAAACCCGCTTAAGACAGAC 1393

QY 3994 TTATCGCACTGGCAGCAGCACTGGTAACAGGATTAAGAGCGGATGTAGCGGT 4053
DB 1394 TTATCGCACTGGCAGCAGCACTGGTAACAGGATTAAGAGCGGATGTAGCGGT 1453

QY 4054 GCTACAGAGTTCTTGAAGTGGTGGCTTAATCTACGGCTTACACTAGAAGAACAGTATTTGGT 4113
DB 1454 GCTACAGAGTTCTTGAAGTGGTGGCTTAATCTACGGCTTACACTAGAAGAACAGTATTTGGT 1513

QY 4114 ATCTGGCTCTGCTGAAGCAGTATCTTCGGAAGAACAGTGTGGTAGCTCTTGATCGGC 4173
DB 1514 ATCTGGCTCTGCTGAAGCAGTATCTTCGGAAGAACAGTGTGGTAGCTCTTGATCGGC 1573

QY 4174 AAAAACAACACCGCTGCTAGCGGTGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGA 4233
DB 1574 AAAAACAACACCGCTGCTAGCGGTGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGA 1633

QY 4234 AAAAAAGGATCTCAAGAAGATCTTTTGTATCTTTTCTACGGGCTCTGA-----CG 4282
DB 1634 AAAAAAGGATCTCAAGAAGATCTTTTGTATCTTTTCTACGGGCTCTGA-----CG 1693

QY 4283 CTGAGAGAACTCGTCAAGAAGCGGATAGAGGCGGATGCGCTCGGAATCGGGAGCGCGCA 4342
DB 1694 CTGAGAGAACTCGTCAAGAAGCGGATAGAGGCGGATGCGCTCGGAATCGGGAGCGCGCA 1753

QY 4343 TACCGTAAAGCAGCAGGAAAGCGGTACGCCCATTCGCGCGCAAGCTCTTTCAGCAATATCAC 4402
DB 1754 TACCGTAAAGCAGCAGGAAAGCGGTACGCCCATTCGCGCGCAAGCTCTTTCAGCAATATCAC 1813

QY 4403 GGSTAGCCAAACGCTATGTCTGTATAGCGGTGCGGCACACACCAGCGCGGCACAGTCGATGA 4462
DB 1814 GGSTAGCCAAACGCTATGTCTGTATAGCGGTGCGGCACACACCAGCGCGGCACAGTCGATGA 1873

QY 4463 ATCCAGAAAGCGGCCATTTTCCACCATGATATTCGCGCAAGCAGGATCGCCATGGGTCA 4522
DB 1874 ATCCAGAAAGCGGCCATTTTCCACCATGATATTCGCGCAAGCAGGATCGCCATGGGTCA 1933

QY 4523 CGACGAGATCTCTCGCGTCTGGGCGATGCGCGCTTTGAGCCCTGGCGAAACAGTTCGCTGGCG 4582
DB 1934 CGACGAGATCTCTCGCGTCTGGGCGATGCGCGCTTTGAGCCCTGGCGAAACAGTTCGCTGGCG 1993

QY 4583 CGAGCCCTGTATGCTCTTCTGTCCAGATCATCTGTATGCAAGAACCGGCTTCCATCCGAG 4642
DB 1994 CGAGCCCTGTATGCTCTTCTGTCCAGATCATCTGTATGCAAGAACCGGCTTCCATCCGAG 2053

QY 4643 TAGCTCTCGCTCGATGCGATGTTTTCGCTTGTGCTGCAATGGGAGGATAGCGCGATCAA 4702
DB 2054 TAGCTCTCGCTCGATGCGATGTTTTCGCTTGTGCTGCAATGGGAGGATAGCGCGATCAA 2113

QY 4703 GCGTATGCAAGCCCGCATTTGCATCAGCCATGATGATGATCTTTCTCGGAGGAGCAAGGT 4762
DB 2114 GCGTATGCAAGCCCGCATTTGCATCAGCCATGATGATGATCTTTCTCGGAGGAGCAAGGT 2173

QY 4763 GAGTACAGGAGATCTCTGCGCGGCACTTTGCGCCCAATAGCAGCCAGTCTCTTCCGCTT 4822
DB 2174 GAGTACAGGAGATCTCTGCGCGGCACTTTGCGCCCAATAGCAGCCAGTCTCTTCCGCTT 2233

QY 4823 CAGTGAACAAGTGCAGCAGCAGTTCGCAAGGAAACCGCTGCGGCGAGCAGCAGATAGCC 4882
DB 2234 CAGTGAACAAGTGCAGCAGCAGTTCGCAAGGAAACCGCTGCGGCGAGCAGCAGATAGCC 2293

QY 4883 GCGCTGCTCTGCTCAGTTCATTTAGGGGCAACCGGACAGGTCGGTCTTTGACAAAAGAA 4942
DB 2294 GCGCTGCTCTGCTCAGTTCATTTAGGGGCAACCGGACAGGTCGGTCTTTGACAAAAGAA 2353

QY 4943 CCGGGCGCCCTGCGCTGACAGCGGAAACACCGCGGCGATCAGAGCAGCGATGCTGTT 5002
DB 2354 CCGGGCGCCCTGCGCTGACAGCGGAAACACCGCGGCGATCAGAGCAGCGATGCTGTT 2413

QY 5003 GTGCCAGTCAATAGCCGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGAATC 5062
DB 2414 GTGCCAGTCAATAGCCGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGAATC 2473

QY 5063 CATTTGTTCAATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5122
DB 2474 CATTTGTTCAATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2533

QY 5123 TGGCCCATCAGATCTCTTGGCGGCAAGAAAGCCATCAGTTTACTTTTTCAGGGGCTTCCAA 5182
DB 2534 TGGCCCATCAGATCTCTTGGCGGCAAGAAAGCCATCAGTTTACTTTTTCAGGGGCTTCCAA 2593

QY 5183 CTTTACAGAGGCGCGCCAGCTGGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5242
DB 2594 CTTTACAGAGGCGCGCCAGCTGGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2653

QY 5243 AGCTAGCAACTGTTGGAGGCGATCG 5271
DB |||||
2654 AGCTAGCAACTGTTGGAGGCGATCG 2682

RESULT 9
US-11-186-282-26
; Sequence 26, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advivis, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 2721
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized pig-GHRH expression plasmid.
US-11-186-282-26

Query Match 32.7%; Score 1771.4; DB 12; Length 2721;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

QY 3454 AGAGCGGTTGCGTATTGGCGCTCTTCGCGTCTTCCTCGCTCACTGACTCGCTCGCGCTCG 3513
DB |||||
859 AGTGAGGTTAAATTCAGAGCTTGGTCTTCGCTTCTCGCTCACTGACTCGCTCGCGCTCG 918
|||

QY 3514 GTGCTTCGCTGCGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACA 3573
DB GTGCTTCGCTGCGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACA 978
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QY 3574 GAATCAGGGATACCGAGGAAGAATGTGAGCAAAAGCGGCAGAAAGGCCAGGAAC 3633
DB GAATCAGGGATACCGAGGAAGAATGTGAGCAAAAGCGGCAGAAAGGCCAGGAAC 1038
|||

QY 3634 CGTAAAGGCGCGTTGCTGGCGTTTTCATAGGCTCGCGCCCTCGACGAGCATCAC 3693
DB CGTAAAGGCGCGTTGCTGGCGTTTTCATAGGCTCGCGCCCTCGACGAGCATCAC 1098
|||

QY 3694 AAAAATCGACGCTCAAGTCAGAGGTGCGAAACCCGACAGACTATATAAGATACAGGCG 3753
DB AAAAATCGACGCTCAAGTCAGAGGTGCGAAACCCGACAGACTATATAAGATACAGGCG 1158
|||

QY 3754 TTTCCCTCGAAGCTCCCTGCTGCTCTCTCTGTTCCGACCTGCGCTTACCGGATAC 3813
DB TTTCCCTCGAAGCTCCCTGCTGCTCTCTCTGTTCCGACCTGCGCTTACCGGATAC 1218
|||

QY 3814 CTGTCGCTTCTTCCTTCGGAAGGTGCGCTTCTCATAGCTCACGCTGTAGGTAT 3873
DB CTGTCGCTTCTTCCTTCGGAAGGTGCGCTTCTCATAGCTCACGCTGTAGGTAT 1278
|||

QY 3874 CTCAAGTTCGCTGATAGGTGCTTCGCTCAAGCTGGGCTGTGTGACAGAACCCCGTTTCA 3933
DB CTCAAGTTCGCTGATAGGTGCTTCGCTCAAGCTGGGCTGTGTGACAGAACCCCGTTTCA 1338
|||

QY 3934 CCGACCGCTGCGCTTATCGGTAACTATGCTCTGAGTCCACCCGTTAAGACAGAC 3993
DB CCGACCGCTGCGCTTATCGGTAACTATGCTCTGAGTCCACCCGTTAAGACAGAC 1398
|||

QY 3994 TTATCGCACTGGCAGCAGCACTGTTAAACAGGATTTAGCAGAGCGAGGTATGTAGGCGGT 4053
DB TTATCGCACTGGCAGCAGCACTGTTAAACAGGATTTAGCAGAGCGAGGTATGTAGGCGGT 1458
|||

QY 4054 GCTACAGAGTTCTTTGAAGTGTGCGCTTAACTACGGCTACACTAGAGAAACAGTATTTGGT 4113
DB GCTACAGAGTTCTTTGAAGTGTGCGCTTAACTACGGCTACACTAGAGAAACAGTATTTGGT 1518
|||

QY 4114 ATCTGCGCTCTGCTGAAGCCAGTTACTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
DB |||||
1519 ATCTGCGCTCTGCTGAAGCCAGTTACTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1578
|||

QY 4174 AAACAAACCAACCGCTGCTAGCGGTGTTTTTTTGTGTAAGCAGCAGATAGCCGAG 4233
DB |||||
1579 AAACAAACCAACCGCTGCTAGCGGTGTTTTTTTGTGTAAGCAGCAGATAGCCGAG 1638
|||

QY 4234 AAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGTCTGA-----CG 4282
DB |||||
1639 AAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGTCTGAAGCTCAGCTAGC 1698
|||

QY 4283 CTCAGAAGAACTCGTCAAGAAGCGGATAGAAAGCGATGCGCTCGCAATCGGAGCGCGA 4342
DB |||||
1699 CTCAGAAGAACTCGTCAAGAAGCGGATAGAAAGCGATGCGCTCGCAATCGGAGCGCGA 1758
|||

QY 4343 TACCGTAAAGCACGAGGAAGCGTCAAGCCATTCGCGCGCAAGCTCTTACAGCAATATCAC 4402
DB |||||
1759 TACCGTAAAGCACGAGGAAGCGGTCAAGCCATTCGCGCGCAAGCTCTTACAGCAATATCAC 1818
|||

QY 4403 GGTAGCCAAACGCTATGTCTGATAGCGGTCCGCCACACCCAGCGGCGCACAGTCCGATGA 4462
DB |||||
1819 GGTAGCCAAACGCTATGTCTGATAGCGGTCCGCCACACCCAGCGGCGCACAGTCCGATGA 1878
|||

QY 4463 ATCCAGAAAGCGCCATTTTCCACATGATATTCGCAAGCAGGACATCCGCATGGGTCA 4522
DB |||||
1879 ATCCAGAAAGCGCCATTTTCCACATGATATTCGCAAGCAGGACATCCGCATGGGTCA 1938
|||

QY 4523 CGACGAGATCCTCGCGTGGGCGATGCGCGCTTGAGCCTTGGCGAAACAGTTTCGGCTGGCG 4582
DB CGACGAGATCCTCGCGTGGGCGATGCGCGCTTGAGCCTTGGCGAAACAGTTTCGGCTGGCG 1998
|||

QY 4583 CGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGAACAGACCGGCTTCCATCCGAG 4642
DB CGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGAACAGACCGGCTTCCATCCGAG 2058
|||

QY 4643 TAGCTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGAGGTAGCCGATCAA 4702
DB TAGCTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGAGGTAGCCGATCAA 2118
|||

QY 4703 GCATATGACGCGCGGATTTGCAATGACCATGATGGAATATTTCTCGGCAAGGACAAAGGT 4762
DB GCATATGACGCGCGGATTTGCAATGACCATGATGGAATATTTCTCGGCAAGGACAAAGGT 2178
|||

QY 4763 GAGATGACAGAGATCTGCGCCCGGCACTTTCGCCCAATAGCAGCAGTCCCTTCCCGCTT 4822
DB GAGATGACAGAGATCTGCGCCCGGCACTTTCGCCCAATAGCAGCAGTCCCTTCCCGCTT 2238
|||

QY 4823 CAGTGACAAACGTCGAGCACAGCTGCGCAAGAAACCGCCGTCGTGGCCAGCACGATAGCC 4882
DB CAGTGACAAACGTCGAGCACAGCTGCGCAAGAAACCGCCGTCGTGGCCAGCACGATAGCC 2298
|||

QY 4883 GCGCTGCTCGTCTCGAGTTCAATTCAGGGCAACCGGACAGGTGCGTCTTGACAAAAAGAA 4942
DB GCGCTGCTCGTCTCGAGTTCAATTCAGGGCAACCGGACAGGTGCGTCTTGACAAAAAGAA 2358
|||

QY 4943 CCGGCGCCCTGCGCTGACAGCGGAAACAGCGGCGCATCAGAGCAGCCGATGCTGTT 5002
DB CCGGCGCCCTGCGCTGACAGCGGAAACAGCGGCGCATCAGAGCAGCCGATGCTGTT 2418
|||

QY 5003 GTGCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGGAGAACTCGCTGCGTGAATC 5062
DB GTGCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGGAGAACTCGCTGCGTGAATC 2478
|||

QY 5063 CATTTGTTCAATCAGCGAAAACGATCCTCATCTGCTCTTGTATCAGATCTTGATCCCC 5122
DB CATTTGTTCAATCAGCGAAAACGATCCTCATCTGCTCTTGTATCAGATCTTGATCCCC 2538
|||

QY 5123 TGGCCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCAA 5182
DB TGGCCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCAA 2598
|||

QY 5183 CCTTACAGAGGGCGCCCGCAGCTGGCAATTTCCGGTTTCGCTTGCTGCCATAAAACCGCCC 5242
|||

Db 2599 CCTTACAGAGGCGCCAGCTGGCAATTCGCGTTGCTGCTCATAAACGCGCC 2658
Qy 5243 AGTCTAGCAACTGTTGGGAAGGCGGATCG 5271
Db 2659 AGTCTAGCAACTGTTGGGAAGGCGGATCG 2687

RESULT 10
US-11-186-282-34
; Sequence 34, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advistsys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 2721
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized Human-GHRH expression plasmid.
US-11-186-282-34

Query Match 32.7%; Score 1771.4; DB 12; Length 2721;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

Qy 3454 AGAGGCGGTTTGCGTATGCGGCTCTTCGCTTCCTCGCTCACTGCTGCTGCGCTCG 3513
Db 859 AGTGAGGTTAATTCAGAGCTTGCTTCGCTTCCTCGCTCACTGCTGCTGCGCTCG 918

Qy 3514 GTGCTTCGCTGCGGAGCGGTATCAGCTCACTCAAGCGGTAAATACGTTATCCACA 3573
Db 919 GTGCTTCGCTGCGGAGCGGTATCAGCTCACTCAAGCGGTAAATACGTTATCCACA 978

Qy 3574 GAATCAGGGATACCCAGGAGGATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 3633
Db 979 GAATCAGGGATACCCAGGAGGATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1038

Qy 3634 CGTAAAGCGCGCTGCTGCGGTTTTCATAGGCTCGCCCTCGCTCACTGAGCATAC 3693
Db 1039 CGTAAAGCGCGCTGCTGCGGTTTTCATAGGCTCGCCCTCGCTCACTGAGCATAC 1098

Qy 3694 AAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAAGATACCAAGCG 3753
Db 1099 AAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAAGATACCAAGCG 1158

Qy 3754 TTTCCCTTCGGAAGCTCCCTGTCGCTCTCTGTTTCGACCTCGCTTACCGATAC 3813
Db 1159 TTTCCCTTCGGAAGCTCCCTGTCGCTCTCTGTTTCGACCTCGCTTACCGATAC 1218

Qy 3814 CTGTCGCTCTTCCTTCGGAAGCTGCGCTTCTCATAGCTCACTGCTAGGTAT 3873
Db 1219 CTGTCGCTCTTCCTTCGGAAGCTGCGCTTCTCATAGCTCACTGCTAGGTAT 1278

Qy 3874 CTCAGTTCGCTGAGTCTGCTCCAAAGCTGGGCTGTGTGACGAACCCCGCTTCAG 3933
Db 1279 CTCAGTTCGCTGAGTCTGCTCCAAAGCTGGGCTGTGTGACGAACCCCGCTTCAG 1338

Qy 3934 CCGACCGCTGCGCTTNTCCGTAATCTGCTTGTAGTCCACCCGCTAAGACAGAC 3993
Db 1339 CCGACCGCTGCGCTTNTCCGTAATCTGCTTGTAGTCCACCCGCTAAGACAGAC 1398

Qy 3994 TTATCCCACTGCGACGACCTGCTAAGAGATTAGCAGCGGAGGTATGTAGCGGT 4053
Db 1399 TTATCCCACTGCGACGACCTGCTAAGAGATTAGCAGCGGAGGTATGTAGCGGT 1458

Qy 4054 GCTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAGAACAGTATTTGTT 4113

Db 1459 GCTTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAGAAACAGTATTTGGT 1518
Qy 4114 ATCTCGCTCTCTGCTGAAGCCAGTTACTTTCGAAAAAGAGTTGTTAGTCTTCTGATCGGC 4173
Db 1519 ATCTCGCTCTCTGCTGAAGCCAGTTACTTTCGAAAAAGAGTTGTTAGTCTTCTGATCGGC 1578
Qy 4174 AAACAAACACCGCTGCTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGAGA 4233
Db 1579 AAACAAACACCGCTGCTAGCGGTGTTTTTTTGTGTTTACAGCAGCAGATTACGCGAGA 1638
Qy 4234 AAAAAGGATCTCAAGAACATCTTTGATCTTTTCTACGGGCTCTGA-----CG 4282
Db 1639 AAAAAGGATCTCAAGAACATCTTTGATCTTTTCTACGGGCTCTGACGCTCAGCTAGCG 1698
Qy 4283 CTCAGAAGAACTCGTCAAGAACGATAGAGCGGATGCGTCGGAATCGGGAGCGGCGA 4342
Db 1699 CTCAGAAGAACTCGTCAAGAACGATAGAGCGGATGCGTCGGAATCGGGAGCGGCGA 1758
Qy 4343 TACCGTAAAGCAGCAGGAAAGCGGTCAAGCCATTCGCGCGCAAGCTCTTCAGCAATATCAC 4402
Db 1759 TACCGTAAAGCAGCAGGAAAGCGGTCAAGCCATTCGCGCGCAAGCTCTTCAGCAATATCAC 1818
Qy 4403 GGGTAGCCAAACGCTATGCTCTGATAGCGGTGCGGCAACCCAGCCGCGCACAAGTCAGTA 4462
Db 1819 GGGTAGCCAAACGCTATGCTCTGATAGCGGTGCGGCAACCCAGCCGCGCACAAGTCAGTA 1878
Qy 4463 ATCCAGAAAGCGGCAATTTCCACCATGATATTCGCAAGCAGGATCGCCATGGTCA 4522
Db 1879 ATCCAGAAAGCGGCAATTTCCACCATGATATTCGCAAGCAGGATCGCCATGGTCA 1938
Qy 4523 CGACGAGATCTTCGCGCTGCGGCTGAGCCCTTGAGCCCTGCGCAACAGTTCGGCTGGCG 4582
Db 1939 CGACGAGATCTTCGCGCTGCGGCTGAGCCCTTGAGCCCTGCGCAACAGTTCGGCTGGCG 1998
Qy 4583 CGAGCCCTGATGCTCTTCGTCAGATCATCTGATGCAAGACCGGCTTCCATCGAG 4642
Db 1999 CGAGCCCTGATGCTCTTCGTCAGATCATCTGATGCAAGACCGGCTTCCATCGAG 2058
Qy 4643 TACGTGCTCGCTCGATGCGATGTTTCGCTGTTGGTGGTGGTGGTGGTGGTGGTGGT 4702
Db 2059 TACGTGCTCGCTCGATGCGATGTTTCGCTGTTGGTGGTGGTGGTGGTGGTGGTGGT 2118
Qy 4703 GGGTATGACGCGCGCATTTGTCATCAGCCATGATGATGATCTTTCTCGGAGGAGCAAGGT 4762
Db 2119 GGGTATGACGCGCGCATTTGTCATCAGCCATGATGATGATCTTTCTCGGAGGAGCAAGGT 2178
Qy 4763 GAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCGCTT 4822
Db 2179 GAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCGCTT 2238
Qy 4823 CAGTGAACAGCTGAGCAGCTGCGCAAGGAAACCGCCGTCGTTGGTGGTGGTGGTGGTGGT 4882
Db 2239 CAGTGAACAGCTGAGCAGCTGCGCAAGGAAACCGCCGTCGTTGGTGGTGGTGGTGGTGGT 2298
Qy 4883 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4942
Db 2299 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2358
Qy 4943 CCGGGCGCCCTGCGCTGATCAGCCGGAACACCGCGGCTCAGAGCAGCGGATGCTGCTT 5002
Db 2359 CCGGGCGCCCTGCGCTGATCAGCCGGAACACCGCGGCTCAGAGCAGCGGATGCTGCTT 2418
Qy 5003 GTGCGCAGTCAATGCGGATAGCTCTCCACCCAGCGCGCGGAGAACCTGCGTGAATC 5062
Db 2419 GTGCGCAGTCAATGCGGATAGCTCTCCACCCAGCGCGCGGAGAACCTGCGTGAATC 2478
Qy 5063 CATCTGTTTCAATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5122
Db 2479 CATCTGTTTCAATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2538
Qy 5123 TCGCGCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTCTTTGCAAGGCTTCCCAA 5182

Db 2539 TGGCCATCAGATCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTGACGGGCTTCCCAA 2598
Qy 5183 CTTTACAGAGGGGCGGCCAGCTGGCAATTCGGTTGCTTGGCTTGTCTGCTCCATAAAACCGCCC 5242
Db 2599 CTTTACAGAGGGGCGGCCAGCTGGCAATTCGGTTGCTTGGCTTGTCTGCTCCATAAAACCGCCC 2658
Qy 5243 AGTCTAGCAACTGTTGGGAAGGCGGATCG 5271
Db 2659 AGTCTAGCAACTGTTGGGAAGGCGGATCG 2687

RESULT 11
US-11-186-282-25
; Sequence 25, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advivys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVS1-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 2725
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized HV-GHRH expression plasmid.
US-11-186-282-25

Query Match 32.7%; Score 1771.4; DB 12; Length 2725;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

Qy 3454 AGAGGGGCTTGGGTATTTGGCGCTCTTCCGCTTCTCTGCTCACTGACTCGCTGCGCTCG 3513
Db 863 AGTGGGGTTAATTTCCAGCTTGGTCTTCCGCTTCTCTGCTCACTGACTCGCTGCGCTCG 922

Qy 3514 GTCGTTGCGTGGCGGAGCGGTATCAGCTCATCTAAAGCGGTATATACGTTATCCACA 3573
Db 923 GTCGTTGCGTGGCGGAGCGGTATCAGCTCATCTAAAGCGGTATATACGTTATCCACA 982

Qy 3574 GAATCAGGGGNTAACGAGAAAGACATCTGAGCAAAAGCCAGCAAAAGGCCAGGAAC 3633
Db 983 GAATCAGGGGNTAACGAGAAAGACATCTGAGCAAAAGCCAGCAAAAGGCCAGGAAC 1042

Qy 3634 CGTAAAAAGCCCGCTTGGCTGGCGTCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAC 3693
Db 1043 CGTAAAAAGCCCGCTTGGCTGGCGTCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAC 1102

Qy 3694 AAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACGAGCG 3753
Db 1103 AAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATATAAAGATACGAGCG 1162

Qy 3754 TTTCCCGCTCGAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC 3813
Db 1163 TTTCCCGCTCGAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC 1222

Qy 3814 CTGTCCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACCGTGTAGGTAT 3873
Db 1223 CTGTCCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACCGTGTAGGTAT 1282

Qy 3874 CTCAGTTGCGTGTAGGTGCTTCCGTTCCAAAGTGGGCTGTGTGCAAGAACCCCGCTTCAG 3933
Db 1283 CTCAGTTGCGTGTAGGTGCTTCCGTTCCAAAGTGGGCTGTGTGCAAGAACCCCGCTTCAG 1342

Qy 3934 CCGACCGCTGGCGCTTATCCGTTAACTATCGTCTTCAGTCCACCCGCGTAAGACACGAC 3993
Db 1343 CCGACCGCTGGCGCTTATCCGTTAACTATCGTCTTCAGTCCACCCGCGTAAGACACGAC 1402

Qy 3994 TTATCGCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGCGAGGTATGTAGGCGGT 4053
Db

Db 1403 TTATCGCCACTGGCAGCAGCCACTGTGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1462
Qy 4054 GCTTACAGAGCTTCTTGAAGTGGTGGCTTAAGCTACGCTACACTAGAGAAGACAGATTATTGGT 4113
Db 1463 GCTTACAGAGCTTCTTGAAGTGGTGGCTTAAGCTACGCTACACTAGAGAAGACAGATTATTGGT 1522
Qy 4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTGGTAGCTCTTTCGATCCGGC 4173
Db 1523 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTGGTAGCTCTTTCGATCCGGC 1582
Qy 4174 AAACAAACCCCGCTGCTAGCGGTGGTTTTTTTGGTAAAGCAGAGATTAGCCGAG 4233
Db 1583 AAACAAACCCCGCTGCTAGCGGTGGTTTTTTTGGTAAAGCAGAGATTAGCCGAG 1642
Qy 4234 AAAAAGGATCTCAAGAAGATCTTTTGATCTTTTCTACGGGGTCTCA-----CG 4282
Db 1643 AAAAAGGATCTCAAGAAGATCTTTTGATCTTTTCTACGGGGTCTGACCGTCACTAGTAGCG 1702
Qy 4283 CTCAGAAAGAACTCGTCAAGAAGSCGATAGAAGCGATGGCTGCGAATCGGGAGCGCGGA 4342
Db 1703 CTCAGAAAGAACTCGTCAAGAAGSCGATAGAAGCGATGGCTGCGAATCGGGAGCGCGGA 1762
Qy 4343 TACCGTAAAGCAGCAGAGAAAGCGGTCAAGCCATTCGCGCCAAAGCTCTTCAGCAATATCAC 4402
Db 1763 TACCGTAAAGCAGCAGAGAAAGCGGTCAAGCCATTCGCGCCAAAGCTCTTCAGCAATATCAC 1822
Qy 4403 GGGTAGCCAAAGCTATGTCTGATAGCGGTTCGCGCACACCCAGCGGCCACAGTCGATGA 4462
Db 1823 GGGTAGCCAAAGCTATGTCTGATAGCGGTTCGCGCACACCCAGCGGCCACAGTCGATGA 1882
Qy 4463 ATCCAGAAAGCGGCCATTTTCCACCATGATATTCCGCAAGCAGGATCGCCATGGGTCA 4522
Db 1883 ATCCAGAAAGCGGCCATTTTCCACCATGATATTCCGCAAGCAGGATCGCCATGGGTCA 1942
Qy 4523 CGACAGATCTTCGCGCTGGGCGATGCGCGCTTTGAGCTTGGCGAAGCAGTTCCGCTGGCG 4582
Db 1943 CGACAGATCTTCGCGCTGGGCGATGCGCGCTTTGAGCTTGGCGAAGCAGTTCCGCTGGCG 2002
Qy 4583 CGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGAACAAGCCGGCTTCCATCCGAG 4642
Db 2003 CGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGAACAAGCCGGCTTCCATCCGAG 2062
Qy 4643 TACGTCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGCAGGTAGCCGATCAA 4702
Db 2063 TACGTCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGCAGGTAGCCGATCAA 2122
Qy 4703 GCGTATGACGCGCGCGGATTTGCAATGAGCTATGATGATCTTCTCGGAGGAGCAAGGT 4762
Db 2123 GCGTATGACGCGCGCGGATTTGCAATGAGCTATGATGATGATCTTCTCGGAGGAGCAAGGT 2182
Qy 4763 GAGATGACAGGAGATCTCGCCCGGCACTTTCGCCCAATAGCAGCAGTCCCTTCCCGCTT 4822
Db 2183 GAGATGACAGGAGATCTCGCCCGGCACTTTCGCCCAATAGCAGCAGTCCCTTCCCGCTT 2242
Qy 4823 CAGTGACAAAGCTCGACGACAGCTGCGCAAGAAAGCCCGCTGGCCAGCCACGATAGCC 4882
Db 2243 CAGTGACAAAGCTCGACGACAGCTGCGCAAGAAAGCCCGCTGGCCAGCCACGATAGCC 2302
Qy 4883 GCGTGCCTCGTCTCGAGTTCAATCAGGGGCAACCGGACAGGTGCTTTCAGAAAAAGAA 4942
Db 2303 GCGTGCCTCGTCTCGAGTTCAATCAGGGGCAACCGGACAGGTGCTTTCAGAAAAAGAA 2362
Qy 4943 CCGGGCGCCCTCGGCTGACAGCGCGGCAACCGCGGCATCAGAGCAGCCGATGTCTGTT 5002
Db 2363 CCGGGCGCCCTCGGCTGACAGCGCGGCAACCGCGGCATCAGAGCAGCCGATGTCTGTT 2422
Qy 5003 GTGCCAGTCAATAGCCGAATAGCTCTTCCACCCAAAGCGCGGAGAACCTTCGCTGCAATC 5062
Db 2423 GTGCCAGTCAATAGCCGAATAGCTCTTCCACCCAAAGCGCGGAGAACCTTCGCTGCAATC 2482
Qy 5063 CATCTGTTCAATCATGCGAAACGATCCTCATCTGCTCTTGTATGATGATCTTGATCCCC 5122
Db 2483 CATCTGTTCAATCATGCGAAACGATCCTCATCTGCTCTTGTATGATGATCTTGATCCCC 2542

Qy	5123	TGCGCCATCAGATCCTTTGGCGGCAAGAAAGCCATCCAGTTTACCTTTCGAGGGCTTCCAA	5182
Db	2543	TGCGCCATCAGATCCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCGAGGGCTTCCAA	2602
Qy	5183	CTTTACAGAGGGCGCCCGCCAGCTGGCAATTCGCGTTTCGCTTGTGTCCATAAACC GCCCC	5242
Db	2603	CTTTACAGAGGGCGCCCGCCAGCTGGCAATTCGCGTTTCGCTTGTGTCCATAAACC GCCCC	2662
Qy	5243	AGTCTACCACTGTTGGGAAGGGCGATCG	5271
Db	2663	AGTCTACCACTGTTGGGAAGGGCGATCG	2691

RESULT 12

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US-11-186-282-32
; Sequence 32, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 32
; LENGTH: 2725
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized chicken-GHRH expression plasmid.
US-11-186-282-32

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Query Match	32.7%;	Score 1771.4;	DB 12;	Length 2725;
Best Local Similarity	98.5%;	Pred. No. 0;		
Matches 1802;	Conservative 0;	Mismatches 16;	Indels 11;	Gaps 1;
Qy	3454	AGAGGGCGTTTTCGGTATTGGCGGCTCTTCGCGCTTCCTCGCTCACTGACTGCTCGCTCGCGCTCG	3513	
Db	863	AGTGAGGGTTAAATTTTCAGAGCTTGCTCTTCGCGCTTCCTCGCTCACTGACTGCTCGCTCGCGCTCG	922	
Qy	3514	GTGCTTCGGCTCGGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACA	3573	
Db	923	GTGCTTCGGCTCGGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACA	982	
Qy	3574	GAATCAGGGGATTAACGACGAGAAAGAAATGTGAGCAAAAGCCAGCAAAAAGGCCAGGAAC	3633	
Db	983	GAATCAGGGGATTAACGACGAGAAAGAAATGTGAGCAAAAGCCAGCAAAAAGGCCAGGAAC	1042	
Qy	3634	CGTAAAAAGCGCGGTGCTGGCGTCTTTTCCATAGGCTCCGCCCTCGACGAGCATCAC	3693	
Db	1043	CGTAAAAAGCGCGGTGCTGGCGTCTTTTCCATAGGCTCCGCCCTCGACGAGCATCAC	1102	
Qy	3694	AAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGCAATATAAAGATACACAGGCG	3753	
Db	1103	AAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGCAATATAAAGATACACAGGCG	1162	
Qy	3754	TTTCCCTCGGAAGCTCCCTCGTCGCTCTCTCTGTTCGACCTTCGCGCTTACCGGATAC	3813	
Db	1163	TTTCCCTCGGAAGCTCCCTCGTCGCTCTCTCTGTTCGACCTTCGCGCTTACCGGATAC	1222	
Qy	3814	CTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	3873	
Db	1223	CTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	1282	
Qy	3874	CTCAGTTTCGGTGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCCCGCTTCAG	3933	
Db	1283	CTCAGTTTCGGTGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCCCGCTTCAG	1342	
Qy	3934	CCCGACCGCTGGCGCTTATCCGGTAACTATCGCTTTGAGTCCAAACCGCGTAAACACGAC	3993	
Db	1343	CCCGACCGCTGGCGCTTATCCGGTAACTATCGCTTTGAGTCCAAACCGCGTAAACACGAC	1402	


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Db      2437 GTGCCCCAGTCATAGCCGATAGCTCTCCACCCAAAGCGCGGAGAACCTCGCTGCAATC 2496
Qy      5063 CATCTTGTTCAATCATCGAAACGATCCTCATCTCTCTCTTGATCAGATCTTGATCCCC 5122
Db      2497 CACTTGTTCAATCATCGAAACGATCCTCATCTCTCTCTTGATCAGATCTTGATCCCC 2556
Qy      5123 TGGCCCATCAGATCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTTCAGGGCTTCCCAA 5182
Db      2557 TGGCCCATCAGATCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTTCAGGGCTTCCCAA 2616
Qy      5183 CCTTACAGAGGGCGCCCGAGCTGGCAATTCGGTTTCGCTTGTGTCATATAAAGCCGCC 5242
Db      2617 CCTTACAGAGGGCGCCCGAGCTGGCAATTCGGTTTCGCTTGTGTCATATAAAGCCGCC 2676
Qy      5243 AGCTAGCAACTGTTGGAAAGGGCGATCG 5271
Db      2677 AGCTAGCAACTGTTGGAAAGGGCGATCG 2705

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RESULT 14

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US-10-523-682-1/c
; Sequence 1, Application US/10523682
; Publication No. US20060014149A1
; GENERAL INFORMATION:
; APPLICANT: Schorr, Kirk
; TITLE OF INVENTION: Methods for rolling circle amplification and signal trapping of
; FILE OF INVENTION: libraries
; FILE REFERENCE: 10292.204-US
; CURRENT APPLICATION NUMBER: US/10/523.682
; CURRENT FILING DATE: 2005-02-01
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 2403
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pMHass5
US-10-523-682-1

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Query Match      25.3%; Score 1372.8; DB 7; Length 2403;
Best Local Similarity 82.4%; Pred. No. 0;
Matches 1759; Conservative 0; Mismatches 172; Indels 203; Gaps 8;

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Qy      3269 TTCTGTGTGAAATTTGTTATCCGCTCACAATTCACACACATACGAGCGGAGCATAA 3328
Db      2193 TTCTGTGTGAAATTTGTTATCCGCTCACAATTCACACACATACGAGCGGAGCATAA 2134
Qy      3329 AGTGTAAAGCTGGGGTGCCCTAATGAGTGAGCTAACTCACAATTAATGCGTTGCGCTCAC 3388
Db      2133 AGTGTAAAGCTGGGGTGCCCTAATGAGTGAGCTAACTCACAATTAATGCGTTGCGCTCAC 2074
Qy      3389 TGCCCGTTTCAGTCGGGAAACCTGTGTCGCGAGTCGATTAATGATCGGCAACGCG 3448
Db      2073 TGCCCGTTTCAGTCGGGAAACCTGTGTCGCGAGTCGATTAATGATCGGCAACGCG 2014
Qy      3449 CGGGAGAGCGGTTTTCGCTATTGGGCGCTTCCGCTTCCGCTCCTCGCTCAGCTCGCTGC 3508
Db      2013 CGGGAGAGCGGTTTTCGCTATTGGGCGCTTCCGCTTCCGCTCCTCGCTCAGCTCGCTGC 1954
Qy      3509 GCTCGGTCGTTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAAGGGGTTAATACGGTTAT 3568
Db      1953 GCTCGGTCGTTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAAGGGGTTAATACGGTTAT 1894
Qy      3569 CCAAGAAATCAGGGGATTAACGAGGAAAGCAATGTGAGCAAAAGGCGCAGCAAAAGGCCA 3628
Db      1893 CCAAGAAATCAGGGGATTAACGAGGAAAGCAATGTGAGCAAAAGGCGCAGCAAAAGGCCA 1863
Qy      3629 GGAACCGTAAAGGGCGGCTTGTGCTGCGCTTTTTCATAGGCTCCGCCGCCCTGACGAGC 3688
Db      1862 -----GGCAAGCGCGTTTTCATAGGCTCCGCCGCCCTGACGAGC 1822

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Qy      3689 ATCAAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACC 3748
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Qy      3749 AGGGGTTTCCCTCGGAAGCTCCCTCGTGGGCTCTCTGTTCCGACCTCGCGCTTACCG 3808
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Db      1702 G-----TGTCAATTCGGCTGTTATGGCGCGTTGTCTCATTCACGC-----C 1660
Qy      3869 GGTATCTCAGTTCGGTGTAGTCTGCTTCCAGCTGGGCTGTGTGCAAGAACCCCGCG 3928
Db      1659 TGACACTCAGTTCGGGTAGGCAAGTTCGCTTCAAGCTGGACTGTATGACAGAACCCCGCG 1600
Qy      3929 TTCAGCCCGACCGCTGGCTTATCCGTTAACTATCTGTTGAGTCCAAACCCCGTAAAGC 3988
Db      1599 TTCAGTCCGACCGCTGGCTTATCCGTTAACTATCTGTTGAGTCCAAACCCCGTAAAGC 1540
Qy      3989 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAG 4048
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Db      1442 TTGGTACTGCGCTCTCTC-CAAGCCAGTTTACCTCGGTTCAAGAGTTGGTAGTTCAGAGA 1384
Qy      4169 CCGGCAAAACAAACACCGCTGTGAGCGGTGTTTGTGTTTTCGCAAGCAGCAGATTACGC 4228
Db      1383 ACCTTCGAAAACCGGCTGCAAGCGGT-----TTTTTCGTTTTTCAGAGCAGAGATTACGC 1326
Qy      4229 GCAGAAAAAAGGATCTCAAGAAGATCTTTTGTATCTTTTCTA----- 4270
Db      1325 GCAGACCAAAACGATCTCAAGAAGATCATCTTATTAAATCAGATAAAATATTTCTAGATTT 1266
Qy      4271 ----- 4270
Db      1265 CAGTGCAATTTATCTCTTCAAAATGTAGCACCTGAAGTCAGCCCCCATACGATATAAGTTGT 1206
Qy      4271 -----CGGGCTCTGACGCTCAGAACCCAGAGTCCGCTCAGAGACTCGT 4297
Db      1205 AATTCATCTGTTGACAGCTTATCATCGCGAACCCAGAGTCCGCTCAGAGACTCGT 1146
Qy      4298 CAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGCGGATACCGTAAAGCA CGA 4357
Db      1145 CAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGCGGATACCGTAAAGCA CGA 1086
Qy      4358 GGNAGCGGTACGCCCATTTGCGCGCAAGCTCTTCAGGAATATCAGGCTAGCCAAACGCTA 4417
Db      1085 GGAAGCGGTACGCCCATTTGCGCGCAAGCTCTTCAGGAATATCAGGCTAGCCAAACGCTA 1026
Qy      4418 TGTCTGTATAGCGGTCCGCGCACACCCAGCGCGGCAAGTGAATCCAGAAAAGCGGC 4477
Db      1025 TGTCTGTATAGCGGTCCGCGCACACCCAGCGCGGCAAGTGAATCCAGAAAAGCGGC 966
Qy      4478 CATTTTCCACCATGATATTTCGCAAGCAGGCAATCGCCATCGGTCACGAGATCTCTCGC 4537
Db      965 CATTTTCCACCATGATATTTCGCAAGCAGGCAATCGCCATCGGTCACGAGATCTCTCGC 906
Qy      4538 CGTGGGCGATGCGCGCTTGTAGCGTGGGAAACGATTTCGGCTGGCGAGGCCCTGTGCT 4597
Db      905 CGTGGGCGATGCGCGCTTGTAGCGTGGGAAACGATTTCGGCTGGCGAGGCCCTGTGCT 846
Qy      4598 CTTTCGTCAGATCATCTGATCGACAAGACCGGCTTCCATCCGAGTACGTCGCTCGCA 4657
Db      845 CTTTCGTCAGATCATCTGATCGACAAGACCGGCTTCCATCCGAGTACGTCGCTCGCA 786
Qy      4658 TGCATGTTTTCGCTTGGTTCGAAATGGGCGAGGTAGCCGAGTCAAGCGTATGACGCGCC 4717

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785 TCGATGTTTCGCTTGGTGTGCGAATGCGCAGGTAGCCGATCAAGCGTATGACGCGCC 726
QY 4718 GCATTGATCAGCCATGATGATATCTTCTCGGAGAGCAAGGTGATGACAGGAGAT 4777
Db 725 GCATTGATCAGCCATGATGATATCTTCTCGGAGAGCAAGGTGATGACAGGAGAT 666
QY 4778 CTTGCCCGCGACCTTGCSCCAATAGCAGCCAGTCCCTTCCCGCTTCAAGTGACAAAGTCGA 4837
Db 665 CTTGCCCGCGACTTCCCAATAGCAGCCAGTCCCTTCCCGCTTCAAGTGACAAAGTCGA 606
QY 4838 GCACAGCTGCGCAGGAACCCCGTGTGCGCAGCCACGATAGCCGCTGCCTCGTCCT 4897
Db 605 GCACAGCTGCGCAGGAACCCCGTGTGCGCAGCCACGATAGCCGCTGCCTCGTCCT 546
QY 4898 GCAGTTCAATCAGGGCACCAGCAGGTGCGTCTTGACAAAAGAACCGGGGCGCCCTGCG 4957
Db 545 GGAGTTCAATCAGGGCACCAGCAGGTGCGTCTTGACAAAAGAACCGGGGCGCCCTGCG 486
QY 4958 CTGACAGCCGGAACACAGCGCGCATCAGACGACCGATTGTGTGTCGCCAGTCATAGC 5017
Db 485 CTGACAGCCGGAACACAGCGCGCATCAGACGACCGATTGTGTGTCGCCAGTCATAGC 426
QY 5018 CGAATAGCCTCTCCACCAAGCGCGCAGAACCTGCGTGCATTCATCTTGTTCATCA 5077
Db 425 CGAATAGCCTCTCCACCAAGCGCGCAGAACCTGCGTGCATTCATCTTGTTCATCA 366
QY 5078 TGGAAACGATCTCATCTGCTCTTGTGATCAGATCTTGATCCCTCGGCCATCAGATCC 5137
Db 365 TGGAAACGATCTCATCTGCTCTTGTGATCAGATCTTGATCCCTCGGCCATCAGATCC 306
QY 5138 TTGGCGGCAGAAAGCCATCCAGTTACTTTTGCAGGGCTTCCCAACCTTACCAGAGGGCG 5197
Db 305 TTGGCGGCAGAAAGCCATCCAGTTACTTTTGCAGGGCTTCCCAACCTTACCAGAGGGCG 246
QY 5198 CCCAGCTGSCAAATTCGGTTCGCTGCTGTGCTCCATAAAACCGCCAGTCTAGCAACTGTT 5257
Db 245 CCCAGCTGSCAAATTCGGTTCGCTGCTGTGCTCCATAAAACCGCCAGTCTAGCTATGCC 186
QY 5258 GGGAGGGCGATCGGTGGGCGCTCTTCGCTATT 5291
Db 185 ATGTAAGCCCACTGCAAGCTACCTGCTTCTCTT 152
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RESULT 15
US-11-094-484-3/c
; Sequence 3, Application US/11094484
; Publication No. US20050261231A1
; GENERAL INFORMATION:
; APPLICANT: KUBO, TATEKI
; APPLICANT: TANAG, MARVIN A.
; APPLICANT: YANO, KENJI
; APPLICANT: MORISHITA, RYUICHI
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR NUCLEIC ACID SEQUENCE TO
; FILE REFERENCE: 074257-0108
; CURRENT APPLICATION NUMBER: US/11/094,484
; CURRENT FILING DATE: 2005-03-31
; PRIOR FILING DATE: 60/557,835
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 5181
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: vector sequence
US-11-094-484-3
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Query Match 24.8%; Score 1347.2; DB 12; Length 5181;

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Best Local Similarity 84.9%; Pred. No. 0;
Matches 1648; Conservative 0; Mismatches 3; Indels 289; Gaps 1;

QY 3595 AAGAACATGTGACCAAAAGCCAGCAAAAGGCCAGGAAACGTAATAAAGCCGGTGTGCTG 3654
Db 5181 AAGAACATGTGACCAAAAGCCAGCAAAAGGCCAGGAAACGTAATAAAGCCGGTGTGCTG 5122
QY 3655 GCCTTTTTCATAGGCTCGGCCCTCGACAGCATCACAAAATCGACGCTCAAGTCAG 3714
Db 5121 GCCTTTTTCATAGGCTCGGCCCTCGACAGCATCACAAAATCGACGCTCAAGTCAG 5062
QY 3715 AGGTGCGGAAAACCCGACAGGACTATATAAGATACACAGCGTTTCCCTCGAAGCTCCCTC 3774
Db 5061 AGGTGCGGAAAACCCGACAGGACTATATAAGATACACAGCGTTTCCCTCGAAGCTCCCTC 5002
QY 3775 GTGCGCTCTCTCTTTCGGACCTTCCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCG 3834
Db 5001 GTGCGCTCTCTCTTTCGGACCTTCCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCG 4942
QY 3835 GGAAGCGTGGCGCTTCTCATAGCTCAACGCTGTAGGTATCTCAGTTCCGTTAGGTCGTT 3894
Db 4941 GGAAGCGTGGCGCTTCTCATAGCTCAACGCTGTAGGTATCTCAGTTCCGTTAGGTCGTT 4882
QY 3895 CGCTCCAAGCTGGGCTGTGTGCAAGAACCCCGTTACGCCGACCGCTCGCTTATPCC 3954
Db 4881 CGCTCCAAGCTGGGCTGTGTGCAAGAACCCCGTTACGCCGACCGCTCGCTTATPCC 4822
QY 3955 GGTAACTATGCTTCTGAGTCCAAACCGGTAAAGACAGACTTATCGCCACTGGCAGAGCC 4014
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QY 4015 ACTGGTAAACAGGATATAGCAGAGCGATGTAGGGGCTGTACAGAGTTCTTGAAGTGG 4074
Db 4761 ACTGGTAAACAGGATATAGCAGAGCGATGTAGGGGCTGTACAGAGTTCTTGAAGTGG 4702
QY 4075 TGGCTTAACCTACCGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA 4134
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QY 4135 GTTACCTTCGAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGC 4194
Db 4641 GTTACCTTCGAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGC 4582
QY 4195 GGTGGTTTTTTTGTGTTGCAAGCAGAGATTAACCGCAGAAAAAAAGGATCTCAAGAGAT 4254
Db 4581 GGTGGTTTTTTTGTGTTGCAAGCAGAGATTAACCGCAGAAAAAAAGGATCTCAAGAGAT 4522
QY 4255 CCTTTGATCTTTTCTACGGGGTCTGACGC----- 4283
Db 4521 CCTTTGATCTTTTCTACGGGGTCTGACGC----- 4462
QY 4284 ----- 4283
Db 4461 TTGCTCATGAGATTATCAAAAAGGATCTTCCACCTAGATCCTTTTAAATTAAAAATGAAGT 4402
QY 4284 ----- 4283
Db 4401 TTTAGCAGCTGCTATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATA 4342
QY 4284 ----- 4283
Db 4341 TTTGAATGATTATTAGAAAAATAAAACAAATAGGGGTTCCGGCGCACATTTCCTCCGAAAAAGTG 4282
QY 4284 ----- 4283
Db 4281 CCACCTGATCGGTGTGAATAACCGCACAGATCGGTAAAGAGAAAAATACCGCATCAGGAA 4222
QY 4284 -----TCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTG 4325
Db 4221 ATTGTAAGCGTTAATAATTTCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTG 4162
QY 4326 CGAATCGGGAGCGCGATACCGTTAAAGCACAGAGAACCGGTACGCCCATTCCTCGCGCCAAAG 4385
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Db 4161 CGAATCGGAGCGCGGATACCGTAAAGCACAGAGAAAGCGGTGAGCCCATTCGCCGCCAAG 4102
 QY CTCTTCAGCAATATCACGGGTAGCCACAGCTATGTCTGATAGCGGTCCGCCACACCCAG 4445
 Db 4101 CTCTTCAGCAATATCACGGGTAGCCACAGCTATGTCTGATAGCGGTCCGCCACACCCAG 4042
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 QY GGCATCGCCATGGGTACAGCAGAGATCCTCGCGTGGGCGATCGCGCCTTGAGCCTGGC 4565
 Db 3981 GGCATCGCCATGGGTACAGCAGAGATCCTCGCGTGGGCGATCGCGCCTTGAGCCTGGC 3922
 QY GAAACAGTTCGGCTGGCGGAGCGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAAG 4625
 Db 3921 GAACAGTTCGGCTGGCGGAGCGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAAG 3862
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 Db 3861 ACCGGCTTCATCCGAGTACGTCGCTCGCTCGATGCGATGTTTCGCTTGGTGGTGAATGG 3802
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 Db 3801 GCGGTAGCCGATCAAGCGTATGACGCGCGCGATTCGATCGATCATCTGATCGACAAG 3742
 QY CTCGGCAGGACGAAGGTGAGTACAGAGAGATCTGCGCCGGCACTTCGCCCAATAGCAG 4805
 Db 3741 CTCGGCAGGACGAAGGTGAGTACAGAGAGATCTGCGCCGGCACTTCGCCCAATAGCAG 3682
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 Db 3681 CCAGTCCCTTCCCGCTTCAGTGACACGTCGAGCAGCTGCGCAAGGAACGCCGCTGCT 3622
 QY GCGCAGCAGCATAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4925
 Db 3621 GCGCAGCAGCATAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3562
 QY GGTCTTGACAAAAGAACCGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4985
 Db 3561 GGTCTTGACAAAAGAACCGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3502
 QY GCAGCCGATTTGCTGTTGTCGCCAGTCATAGCCGAATAGCCTCTCCACCCCAAGCGGCCG 5045
 Db 3501 GCAGCCGATTTGCTGTTGTCGCCAGTCATAGCCGAATAGCCTCTCCACCCCAAGCGGCCG 3442
 QY AGAACCTGCGTGAATCCATCTTGTTCATATGCGAAGAGATCCTGCTGCTGCTGCTGCTG 5105
 Db 3441 AGAACCTGCGTGAATCCATCTTGTTCATATGCGAAGAGATCCTGCTGCTGCTGCTGCTG 3382
 QY ATCAGATCTTTGATCCCTGCGCATCAGATCCTTGGCGCAAGAAAGCCATCCAGTTTAC 5165
 Db 3381 ATCAGATCTTTGATCCCTGCGCATCAGATCCTTGGCGCAAGAAAGCCATCCAGTTTAC 3322
 QY TTTGCGGGCTTCCCAACCTTACGAGGGCGGCCCAAGCTGGCAATTCGGTTTCGCTTGC 5225
 Db 3321 TTTGCGGGCTTCCCAACCTTACGAGGGCGGCCCAAGCTGGCAATTCGGTTTCGCTTGC 3262
 QY TGTCCATAAAACCGCCAGT 5245
 Db 3261 TGTCCATAAAACCGCCAGT 3242

Search completed: February 20, 2006, 19:49:16
 Job time : 1300 secs

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Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 18:48:03 ; Search time 25985 Seconds
(without alignments)
11863.076 Million cell updates/sec

Title: US-10-798-896-1

Perfect score: 5423
Sequence: 1 ccaccgcgtggcgccgtc.....ctataggcgaattggagct 5423

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.in.*
- 3: gb.env.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: gb.htg.*
- 15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5423	100.0	5423	6	CQ877110	Sequence
2	2237	41.3	2237	6	CQ877114	Sequence
3	2218	40.9	3599	6	BD063790	Insulin-1
4	2218	40.9	3599	6	BD069041	Treatment
5	2218	40.9	3803	6	CQ877111	Sequence
6	2215.8	40.9	3600	6	BD063789	Insulin-1
7	2215.8	40.9	3600	6	BD069040	Treatment
8	2211.6	40.8	3558	6	CQ854738	Sequence
9	2160	39.8	3534	6	CQ854723	Sequence
10	2160	39.8	3534	6	CQ854724	Sequence
11	2160	39.8	3534	6	CQ854725	Sequence
12	2160	39.8	3534	6	CQ854726	Sequence
13	2160	39.8	3534	6	CQ854727	Sequence
14	2160	39.8	3534	6	CQ854741	Sequence
15	2160	39.8	3534	6	CQ903781	Sequence
16	2160	39.8	3534	6	CQ903782	Sequence
17	2160	39.8	3534	6	CQ903783	Sequence
18	2160	39.8	3534	6	CQ903784	Sequence

19	2160	39.8	3534	6	CQ903785	Sequence
20	2160	39.8	3534	6	CS131823	Sequence
21	2059	38.0	5966	6	BD136050	Interfero
22	1989	36.7	4496	6	AX249945	Sequence
23	1988.8	36.7	3426	6	BD136049	Interfero
24	1988.8	36.7	3589	6	BD136051	Interfero
25	1988.8	36.7	3589	6	AX249943	Sequence
26	1988.8	36.7	3609	6	AX249944	Sequence
27	1988.8	36.7	4855	6	CQ854739	Sequence
28	1788.4	33.0	3100	6	AX451645	Sequence
29	1788.4	33.0	4276	6	AX249946	Sequence
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31	1773	32.7	2722	6	CS131824	Sequence
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41	1771.4	32.7	2716	6	CS131832	Sequence
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43	1771.4	32.7	2725	6	CQ854742	Sequence
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ALIGNMENTS

RESULT 1	CQ877110	CQ877110	5423 bp	DNA	linear	PAT 04-OCT-2004
LOCUS	Sequence 1 from Patent WO2004081040.					
DEFINITION	CQ877110					
ACCESSION	CQ877110.1	GI:53790386				
VERSION						
KEYWORDS	synthetic construct					
SOURCE	other sequences; artificial sequences.					
ORGANISM	1					
REFERENCE	Rabinovsky, E.D. and Draghia-Akli, R.					
AUTHORS	Insulin-like growth factor (igf-i) plasmid-mediated supplementation					
TITLE	for therapeutic applications					
JOURNAL	Patent: WO 2004081040-A 1 23-SEP-2004;					
FEATURES	Advisys, Inc. (US); BAYLOR COLLEGE OF MEDICINE (US)					
source	Location/Qualifiers					
	1. .5423					
	/organism="synthetic construct"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32630"					
	/note="Nucleic acid sequence for the pAV2001 plasmid."					

ORIGIN	Query Match	100.0%;	Score 5423;	DB 6;	Length 5423;
	Best Local Similarity	100.0%;	Pred. No. 0;		
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				Indels	0;
				Gaps	0;
Qy	1	CCACCGCGTGGCGCGCGTCCGCCCTCGGCACCATCTCAGACACCCAAATATGGCGAC	60		
Db	1	CCACCGCGTGGCGCGCGTCCGCCCTCGGCACCATCTCAGACACCCAAATATGGCGAC	60		
Qy	61	GGGTGAGGAATGTGGGGAGTTATTTTAGAGCGGTGAGGAGGTGGCGGCGGACGAGT	120		
Db	61	GGGTGAGGAATGTGGGGAGTTATTTTAGAGCGGTGAGGAGGTGGCGGCGGACGAGT	120		
Qy	121	GTGGCGCTCTAAATAAATACTCCCGGAGTTATTTTAGAGCGGAGGAATGTGGACACC	180		
Db	121	GTGGCGCTCTAAATAAATACTCCCGGAGTTATTTTAGAGCGGAGGAATGTGGACACC	180		
Qy	181	CAATATGGCGACGGTTCTTCACCCGTCGCCATATTTGGGTGTCGCCCTCGGCCGGGC	240		

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Q	y		2914	TCAGGGTCAGCATCCTCAGCATCTAGGGATGTGCATAATGTGTGATGGTGACACTTTTAGA	2973
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Q	y		2974	GAACTGCTTTGATTCCCAGGGCTTTCCCTCTCTTTCATGTCAGGGCTCACTATCAGGCCCT	3033
D	b		2041	GAACTGCTTTGATTCCCAGGGCTTTCCCTCTCTTTCATGTCAGGGCTCACTATCAGGCCCT	2100
Q	y		3034	GAAGAGTCCAACCTTCTGAACCTCCAGCACCGTCTGCTCTGGTAGGGCTGTCCATAGAGG	3093
D	b		2101	GAAGAGTCCAACCTTCTGAACCTCCAGCACCGTCTGCTCTGGTAGGGCTGTCCATAGAGG	2160
Q	y		3094	CCACAGGGACTGTAGCCAGGCATGACCTTTTCCAGCCGGTGTCTGAATCCAGCACTGGT	3153
D	b		2161	CCACAGGGACTGTAGCCAGGCATGACCTTTTCCAGCCGGTGTCTGAATCCAGCACTGGT	2220
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LOCUS					
DEFINITION Insulin-like growth factor I(IGF)-1 expression system and methods of use.					
ACCESSION BD063790					
VERSION BD063790.1 GI:22609393					
KEYWORDS JP 2001505435-A/3.					
SOURCE synthetic construct					
ORGANISM other sequences; artificial sequences.					
REFERENCE 1 (bases 1 to 3599)					
AUTHORS Coleman,M., Schwartz,R. and Demayo,F.J.					
TITLE Insulin-like growth factor I(IGF)-1 expression system and methods of use.					
JOURNAL Patent: JP 2001505435-A 3 24-APR-2001;					
COMMENT BARENTIS INC,BAYLOR COLLEGE OF MEDICINE					
PN JP 2001505435-A/3					
PD 24-APR-2001					
PF 01-DEC-1997 JP 1998525696					
PR 02-DEC-1996 US 60/031539,19-NOV-1997 US 08/974572 PI					
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Best Local Similarity 99.8%; Pred. No. 0;					
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;					
Q	y		3190	GAGCCAGGGAAACAAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG	3249
D	b		3	GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG	62
Q	y		3250	TAAATCATGCTPAGCTGTTTTCTGTGTGAAATTTGTTATCCGCTCAAAATTCACACAAC	3309
D	b		63	TAAATCATGCTPAGCTGTTTTCTGTGTGAAATTTGTTATCCGCTCAAAATTCACACAAC	122
Q	y		3310	ATACGAGCCGGAAGCATAAAGTCTAAAGCTCTGGGTGTCCTTAATGAGTGAGCTAACTACA	3369
D	b		123	ATACGAGCCGGAAGCATAAAGTCTAAAGCTCTGGGTGTCCTTAATGAGTGAGCTAACTACA	182
Q	y		3370	TTAANTCGCTTGGCTCACTGCCCGCTTTTCCAGCTCGGGAACCTGTCTGTCGCCAGCTGCAT	3429

183	Db	TTAATTGCGTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCAT	242
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243	Db	TAATGAATCGGCCAAACGCGCGGGAGAGGGGTTTCGGTATTTGGGGCGCTCTTCCGCTTCC	302
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303	Db	TCGCTCACTCACTCGCTCGCTCGCTCGCTCGCTCGCGCTCGCGACGCGTATCAGCTCACTCA	362
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723	Db	TGTTGTCACGAAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGATAACTATCGTCTT	782
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783	Db	GAGTCCAAACCGGTAAAGACAGCTTATCGCACTGGCAGCAGGCCTGTGTACAGGATT	842
4030	Qy	AGCAGACGAGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCTTAACCTACGGC	4089
843	Db	AGCAGACGAGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCTTAACCTACGGC	902
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903	Db	TACACTAGAAGAAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACTCTGGAAAA	962
4150	Qy	AGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGTTTTTGT	4209
963	Db	AGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGTTTTTGT	1022
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4390	Qy	TCAGCAATATCACGGGTAGCCAAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCG	4449
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Db	1263	CCACAGTCGATGAATCCAGAAAAGCGGCATTTTTCACCAATGATATATTCGCGCAAGCAGGCA	1322
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Db	1323	TCGCCATGGGTACAGCAGATCCTCGCGTTCGGGCAATGCGCCCTTGAGCCCTGGCGGAAC	1382
Qy	4570	AGTTTCCGCTGGCGGAGCCCTGATGCTTTTCGTTCAGATCATCTGTATCGACAGACCG	4629
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Qy	4810	TCCCTTCCCGCTTCAGTGACAACGTGCAGCACAGCTCGCAAGAAAGCCCGCTCGTGCC	4869
Db	1623	TCCCTTCCCGCTTCAGTGACAACGTGCAGCACAGCTCGCAAGAAAGCCCGCTCGTGCC	1682
Qy	4870	AGCCACGATAGCCGCTGCTCTGTCAGTTTCATTCAGGGGACCGGACAGGTTCGGTC	4929
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Qy	5050	CCTCGTCGCAATCCATCTTGTTCAATCATGCGAAACGATCTCATCTGCTCTTGATCA	5109
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Qy	5110	GATCTTGATCCCTTCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG	5169
Db	1923	GATCTTGATCCCTTCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG	1982
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LOCUS	
DEFINITION	BD069041 Treatment for urinary incontinence using gene therapy techniques.
ACCESSION	BD069041
VERSION	BD069041.1 GI:22614644
	3599 bp DNA linear PAT 27-AUG-2002

KEYWORDS JP 2001511154-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 3599)
AUTHORS Coleman,M. for urinary incontinence using gene therapy techniques
JOURNAL Patent: JP 2001511154-A 3 07-AUG-2001;
BARENTIS INC
COMMENT OS Unidentified
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PD 07-AUG-2001
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LOCUS CQ877111 3803 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 2 from Patent WO2004081040.
ACCESSION CQ877111
VERSION CQ877111.1 GI:53790387
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Rabinovsky,E.D. and Draghia-Akli,R.
TITLE Insulin-like growth factor (Igf-I) plasmid-mediated supplementation
for therapeutic applications
JOURNAL Patent: WO 2004081040-A 2 23-SEP-2004;
Advisys, Inc. (US); BAYLOR COLLEGE OF MEDICINE (US)
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Location/Qualifiers
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ORIGIN

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Db 1570 GAGGCGGGGGCCCGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCAGCTTGGCG 1629
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Db 3790 GCGCAATTGGAGCT 3803
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LOCUS
DEFINITION
BD063789 Insulin-like growth factor I (IGF)-1 expression system and methods of use.
ACCESSION BD063789.1 GI:22609392
VERSION JP 2001505435-A/2
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 3600)
AUTHORS Coleman, M., Schwartz, R. and Demayo, F.J.
TITLE Insulin-like growth factor I (IGF)-1 expression system and methods of use.
JOURNAL Patent: JP 2001505435-A 2 24-APR-2001;
COMMENT BARENTIS INC, BAYLOR COLLEGE OF MEDICINE
PN JP 2001505435-A/2
PD 24-APR-2001
PR 01-DEC-1997 JP 1998525696
PR 02-DEC-1996 US 60/031539, 19-NOV-1997 US 08/974572 P1
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C12N15/85, C07K14/65, A61K48/00, A01K67/027
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CC Topology: Linear;
FH Key Location/Qualifiers.
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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LOCUS	BD069040		linear
DEFINITION	Treatment for urinary incontinence using gene therapy techniques.		
ACCESSION	BD069040		PAT 27-AUG-2002
VERSION	BD069040.1	GI:22614643	
KEYWORDS	JP 2001511154-A/2.		
SOURCE	unidentified		
ORGANISM	unidentified		
REFERENCE	1 (bases 1 to 3600)		
AUTHORS	Coleman,M.		
TITLE	Treatment for urinary incontinence using gene therapy techniques		
JOURNAL	Patent: JP 2001511154-A 2 07-AUG-2001;		
COMMENT	BARENTIS INC		
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	PN	JP 2001511154-A/2	
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	PR	04-FEB-1997	US 60/036862
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	PC	A61k48/00	
	CC	Strandedness: Single;	
	CC	Topology: Linear;	
	CC	Treatment for urinary incontinence using gene therapy	CC
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FEATURES			Location/Qualifiers

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ACCESSION CQ854738
VERSION CQ854738.1 GI:51510298
KEYWORDS
SOURCE synthetic construct
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other sequences; artificial sequences.

REFERENCE 1
AUTHORS Brown, P.A., Draghia-Akli, R. and Carpenter, R.H.
TITLE Reducing culling in herd animals growth hormone releasing hormone (ghrh)
JOURNAL Patent: WO 2004067719-A 26 12-AUG-2004;
Adviseys, Inc. (US)
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ACCESSION	CQ854723
VERSION	CQ854723.1 GI:51510283
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SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1. Brown, P.A., Draghia-Akli, R. and Carpenter, R.H.
TITLE	Reducing culling in herd animals growth hormone releasing hormone(ghrh)
JOURNAL	Patent: WO 2004067719-A 11 12-AUG-2004;
FEATURES	Advisys, Inc. (US)
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LOCUS
DEFINITION Sequence 12 from Patent WO2004067719.
ACCESSION CO854724
VERSION CO854724.1 GI:51510284
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
TITLE Reducing culling in herd animals growth hormone releasing hormone(ghrh)
JOURNAL Patent: WO 2004067719-A 12 12-AUG-2004;
Adviseys, Inc. (US)
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RESULT 12
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LOCUS

Sequence 14 from Patent WO2004067719.

linear

PAT 23-AUG-2004

ACCESSION C0854726
VERSION Q0854726.1 GI:51510286
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brown, P.A., Draghia-Akli, R. and Carpenter, R.H.
TITLE Reducing culling in herd animals growth hormone releasing hormone(ghrh)
JOURNAL Patent: WO 2004067719-A 14 12-AUG-2004;
Adviseys, Inc. (US);
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VERSION				CO854727.1 GI:51510287
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SOURCE				synthetic construct
ORGANISM				other sequences; artificial sequences.
REFERENCE				1
AUTHORS				Brown, P.A., Draghia-Akli, R. and Carpenter, R.H.
TITLE				Reducing culling in herd animals growth hormone releasing hormone(ghrh)
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Best Local Similarity				99.5%; Pred. No. 0;
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REFERENCE 1
AUTHORS Draghia-Akli, R., Scott, C. and Brown, P. A.
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JOURNAL Patent: WO 2004093920-A 11 04-NOV-2004;
Adviseys, Inc. (US)
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Db	2679	TCGCCATGGGTACGACAGATCCTCCCGCTCGGGCATGCGCGCTTTGACCTTGGCGAAC	2738
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Job time : 25991 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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12940.433 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	2218	40.9	3599	2 AAV50428	Aav50428 Plasmid p
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8	2215.8	40.9	3600	2 AAV50427	Aav50427 Plasmid p
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17	2160	39.8	3534	9 AAL62058	Aal62058 pSP-HV-GH
18	2160	39.8	3534	9 AAL62061	Aal62061 15/27/28-
19	2160	39.8	3534	9 AAL60444	Aal60444 TI-GHRH p

20	2160	39.8	3534	9 AAL60445	Aal60445 TV-GHRH p
21	2160	39.8	3534	9 AAL60446	Aal60446 15/27/28
22	2160	39.8	3534	9 AAL60443	Aal60443 pSP-HV-GH
23	2160	39.8	3534	9 AAL60447	Aal60447 Wild-type
24	2160	39.8	3534	10 ACF04661	Acf04661 Wildtype
25	2160	39.8	3534	10 ACF04660	Acf04660 15/27/28
26	2160	39.8	3534	10 ACF04657	Acf04657 HV-GHRH o
27	2160	39.8	3534	10 ACF04659	Acf04659 TV-GHRH o
28	2160	39.8	3534	10 ACF04658	Acf04658 TI-GHRH o
29	2160	39.8	3534	12 ADF90306	Adf90306 Wild type
30	2160	39.8	3534	12 ADF90302	Adf90302 HV-GHRH p
31	2160	39.8	3534	12 ADF90304	Adf90304 TV-GHRH p
32	2160	39.8	3534	12 ADF90305	Adf90305 15/27/28
33	2160	39.8	3534	12 ADF90303	Adf90303 TI-GHRH p
34	2160	39.8	3534	12 ADL70452	Adl70452 Protease
35	2160	39.8	3534	12 ADL70453	Adl70453 Protease
36	2160	39.8	3534	12 ADL70454	Adl70454 Protease
37	2160	39.8	3534	12 ADO31099	Ado31099 Cardiac s
38	2160	39.8	3534	12 ADO31100	Ado31100 Cardiac s
39	2160	39.8	3534	12 ADO31098	Ado31098 Cardiac s
40	2160	39.8	3534	12 ADO31101	Ado31101 Cardiac s
41	2160	39.8	3534	13 ADR23409	Adr23409 Codon opt
42	2160	39.8	3534	13 ADR23393	Adr23393 TI-GHRH p
43	2160	39.8	3534	13 ADR23394	Adr23394 TV-GHRH p
44	2160	39.8	3534	13 ADR23395	Adr23395 15/27/28-
45	2160	39.8	3534	13 ADR23392	Adr23392 Plasmid p

ALIGNMENTS

RESULT 1

ADS73973

ID ADS73973 standard; DNA; 5423 BP.

XX ADS73973;

DT 16-DEC-2004 (first entry)

DE Plasmid pAV2001 nucleotide sequence.

XX IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
KW vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
KW cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX Synthetic.
OS
XX WO2004081040-A2.
XX
XX
PD 23-SEP-2004.
XX
XX 11-MAR-2004; 2004WO-US007295.
XX
XX 12-MAR-2003; 2003US-0454079P.
XX
XX (ADVI-) ADVISYS INC.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX Rabinovsky ED, Draghia-Akli R;
XX WPI; 2004-668935/65.
XX
XX New isolated nucleic acid expression construct having a myogenic
PT promoter, a nucleic acid sequence encoding IGF-I, and a 3'UTR, useful
PT for treating diabetes, ischemic heart and cerebrovascular disease.
XX
XX Claim 11; SEQ ID NO 1; 104pp; English.
XX
XX The invention relates to an isolated nucleic acid expression construct
CC comprising a myogenic promoter, a nucleic acid sequence encoding an
CC insulin-like growth factor I (IGF-I) or its functional biological
CC equivalent, and a 3' untranslated region (3'UTR), which has in vivo

expression activity for the encoded IGF-1 in a tissue. The myogenic promoter in the isolated nucleic acid expression construct comprises a transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The 3'-UTR is from a skeletal alpha actin gene or from a human growth hormone. The expression construct further comprises transfection-facilitating vector system that is a plasmid, a viral vector, a liposome, or a cationic lipid. The isolated nucleic acid expression construct also comprises a transfection-facilitating polypeptide having a charged polypeptide and/or poly-L-glutamate. The construct is useful in a method for stimulating angiogenesis, or stimulating myogenesis, or elevating levels of an angiogenic factor, or stimulating endogenous production of an angiopoietin, or treating a muscular or vascular complications of diabetes in a subject. The angiogenic factor comprises a vascular endothelial growth factor (VEGF) or VEGF receptor. The methods and compositions of the present invention are useful for the prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the IGF-1, such as diabetes mellitus, ischemic heart disease, diabetic retinopathy and cerebrovascular disease. The present sequence represents the nucleotide sequence of a plasmid pAV2001, a specific example of the isolated nucleic acid expression construct of the invention.

XX Sequence 5423 BP; 1219 A; 1475 C; 1474 G; 1255 T; 0 U; 0 Other;

Query Match 100.0%; Score 5423; DB 13; Length 5423;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCGGGTGGGGCGTCCGCCCTCGGCACCATCTCCAGACCCAAATATGGCGAC 60
DB 1 CCACCGGGTGGGGCGTCCGCCCTCGGCACCATCTCCAGACCCAAATATGGCGAC 60

QY 61 GGGTGAGGAATGGTGGGGAGTTATTTTAGAGCGGTGAGAGGTGGCGCAGCAGGT 120
DB 61 GGGTGAGGAATGGTGGGGAGTTATTTTAGAGCGGTGAGAGGTGGCGCAGCAGGT 120

QY 121 GTTGGCGCTCTAAATAAATCTCCGGGAGTTATTTTAGAGCGGAGGAATGGTGACAC 180
DB 121 GTTGGCGCTCTAAATAAATCTCCGGGAGTTATTTTAGAGCGGAGGAATGGTGACAC 180

QY 181 CAAATATGGGACGGTTCCTCACCCGTCCGATATTTGGGTGTCGCCCTCGGCGGGG 240
DB 181 CAAATATGGGACGGTTCCTCACCCGTCCGATATTTGGGTGTCGCCCTCGGCGGGG 240

QY 241 CGCATTCCTGGGGCGGGGGTCTCCGCCCGCTCGATAAAGGCTCGGGGGCGGC 300
DB 241 CGCATTCCTGGGGCGGGGGTCTCCGCCCGCTCGATAAAGGCTCGGGGGCGGC 300

QY 301 GGGGCGCCACGAGCTACCCGAGGAGCGGAGGCGCAAGCTCTAGAACTAGTGATCCC 360
DB 301 GGGGCGCCACGAGCTACCCGAGGAGCGGAGGCGCAAGCTCTAGAACTAGTGATCCC 360

QY 361 AAGGCCCAATCCCGCAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCCATGGGA 420
DB 361 AAGGCCCAATCCCGCAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCCATGGGA 420

QY 421 AAAATCGAGCTCTTCCAAATTTAATTTAAGTGTGCTTTTGTGATTTCTGAAGGTG 480
DB 421 AAAATCGAGCTCTTCCAAATTTAATTTAAGTGTGCTTTTGTGATTTCTGAAGGTG 480

QY 481 AAGATGACACCATGTCTCTCCGATCTCTTCTACCTGGGGTGTGCTCTCACCTTC 540
DB 481 AAGATGACACCATGTCTCTCCGATCTCTTCTACCTGGGGTGTGCTCTCACCTTC 540

QY 541 ACCAGCTCTGCCAGGCTGGACCGGAGAGCTCTCGGGGGTGAGCTGGTGATGCTCTT 600
DB 541 ACCAGCTCTGCCAGGCTGGACCGGAGAGCTCTCGGGGGTGAGCTGGTGATGCTCTT 600

QY 601 CAGTCTGTGTGAGAGCAGGGGCTTTTATTTCAACAGCCCAAGGGTATGGCTCCAGC 660
DB 601 CAGTCTGTGTGAGAGCAGGGGCTTTTATTTCAACAGCCCAAGGGTATGGCTCCAGC 660

QY 661 AGTCGGAGGGCGCTCAGACACAGGATCGTGATGAGTGTCTCTCCGAGCTGTGATCTA 720

DB 661 AGTCGGAGGGCGCTCAGACACAGGATCGTGATGAGTGTCTCTCCGAGCTGTGATCTA 720

QY 721 AGGAGGCTGGAGATGTTATTTGGCACCCCTCAGCCTGCCAAGTCAGTCGCTCTGTCCT 780
DB 721 AGGAGGCTGGAGATGTTATTTGGCACCCCTCAGCCTGCCAAGTCAGTCGCTCTGTCCT 780

QY 781 GCCCAGCGGCACACCGACATGCCCAAGACCCAGAGGAAGTACATTTGAAGAACGCAAGT 840
DB 781 GCCCAGCGGCACACCGACATGCCCAAGACCCAGAGGAAGTACATTTGAAGAACGCAAGT 840

QY 841 AGAGGAGTGCAGGAAACAAAGACTACAGGATGTAGAGAACCCCTCTCTGAGAGTGGA 900
DB 841 AGAGGAGTGCAGGAAACAAAGACTACAGGATGTAGAGAACCCCTCTCTGAGAGTGGA 900

QY 901 GTGACATGCCACCGAGGATCCCGGGCTGCGAGGAATTCGATGGGCCATCCATTGTGTC 960
DB 901 GTGACATGCCACCGAGGATCCCGGGCTGCGAGGAATTCGATGGGCCATCCATTGTGTC 960

QY 961 CCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACACACTCAGGATGACAA 1020
DB 961 CCGTAAATGCTTCTAAACATGTTTACATGATCACTTTGCCAACACACTCAGGATGACAA 1020

QY 1021 TCTGTAGGTTCCAGGCTGCTGAGGACCTCCACAGCCATGCAACTTTCTATTGTGTAAC 1080
DB 1021 TCTGTAGGTTCCAGGCTGCTGAGGACCTCCACAGCCATGCAACTTTCTATTGTGTAAC 1080

QY 1081 AATTTCTGGTACTGTTGCTGCAAGCTCCATGTCACAGTGTATGTAAGTGATACATA 1140
DB 1081 AATTTCTGGTACTGTTGCTGCAAGCTCCATGTCACAGTGTATGTAAGTGATACATA 1140

QY 1141 AATTAATTTATTTTACTCGTTTGTGTTTAAACCAATGCCCTGTGGAAGGAAC 1200
DB 1141 AATTAATTTATTTTACTCGTTTGTGTTTAAACCAATGCCCTGTGGAAGGAAC 1200

QY 1201 ATAAACTTCAAGAAGCATTTAAATCATAGTCACTTGTGCACACCCCTAATGCAATGTT 1260
DB 1201 ATAAACTTCAAGAAGCATTTAAATCATAGTCACTTGTGCACACCCCTAATGCAATGTT 1260

QY 1261 TCTGTCACTATTTCCCTGGGCTCTTCCATCTCTCGTGCACCTGGGACTGGGTGCTGGGC 1320
DB 1261 TCTGTCACTATTTCCCTGGGCTCTTCCATCTCTCGTGCACCTGGGACTGGGTGCTGGGC 1320

QY 1321 TGGGAGCAGGGGTGGGGCTCTCCAGGAGAGATGGCATGGGAGAGTGTATGGGATCTG 1380
DB 1321 TGGGAGCAGGGGTGGGGCTCTCCAGGAGAGATGGCATGGGAGAGTGTATGGGATCTG 1380

QY 1381 CTGGGGGGGGGACTCACCTCTGTGGCTGCAAGAACCCATTTGGTGCAGAGAGCAG 1440
DB 1381 CTGGGGGGGGGACTCACCTCTGTGGCTGCAAGAACCCATTTGGTGCAGAGAGCAG 1440

QY 1441 CTTGGGATGCCATGACACGGGCAACCATGTCACCGTGTCTCCCATGCCAGTACGGGA 1500
DB 1441 CTTGGGATGCCATGACACGGGCAACCATGTCACCGTGTCTCCCATGCCAGTACGGGA 1500

QY 1501 AAGGTTTACGAGCGCGTTCATTTCTAGCTTTGGAAGATTTTGTGGGCTCAGCCTGCC 1560
DB 1501 AAGGTTTACGAGCGCGTTCATTTCTAGCTTTGGAAGATTTTGTGGGCTCAGCCTGCC 1560

QY 1561 AGAGCAGTAGCCAGGCAATGCTGTGACCTCCAGCTGTGATGGAAGAGCAAGGCTGC 1620
DB 1561 AGAGCAGTAGCCAGGCAATGCTGTGACCTCCAGCTGTGATGGAAGAGCAAGGCTGC 1620

QY 1621 AGCTGAGGCCAGGTGTGGGCAAGGTTAAATTAAGAGCTTCCACTCCATTATGAAA 1680
DB 1621 AGCTGAGGCCAGGTGTGGGCAAGGTTAAATTAAGAGCTTCCACTCCATTATGAAA 1680

QY 1681 GCCCTCTGCACTCACCTGTCTCCCTGGGCTGGGGGCGAGCCAGGGCCACTTCTCCACCCC 1740
DB 1681 GCCCTCTGCACTCACCTGTCTCCCTGGGCTGGGGGCGAGCCAGGGCCACTTCTCCACCCC 1740

QY 1741 ACCTGACACAAAGGCTTTGCCCTGCAAGCAGGACTCTCTGTGGGCGCAGAGCTCTTATA 1800

Db 1741 ACCTGACACAAAGGCTTTGCCCTGTCACAGCAGGAGACCTCTCTGTGGCCACAGACTCTTTATA 1800
Qy 1801 GATTCGCTGTGCCCTAGGAGACAGAGGGGCTTTCCCTGCTGCGCTTCTGGCCCGCGCA 1860
Db 1801 GATTCGCTGTGCCCTAGGAGACAGAGGGGCTTTCCCTGCTGCGCTTCTGGCCCGCGCA 1860
Qy 1861 CACTGCAAGAGCTGCCCTATCTGCTCCTCTTAGATGGTCTTGGCAGGAAAGCTGCACATT 1920
Db 1861 CACTGCAAGAGCTGCCCTATCTGCTCCTCTTAGATGGTCTTGGCAGGAAAGCTGCACATT 1920
Qy 1921 GGCTTGGGGCTGATCCCATATACACCTGCACTAGTGGGACAGCACTGCTGGAGAAAGATG 1980
Db 1921 GGCTTGGGGCTGATCCCATATACACCTGCACTAGTGGGACAGCACTGCTGGAGAAAGATG 1980
Qy 1981 ATTTTCAACTGAACCTTACTATCAAGCAGGCTTATGCTTTATTTGATGGTGTAAAGAT 2040
Db 1981 ATTTTCAACTGAACCTTACTATCAAGCAGGCTTATGCTTTATTTGATGGTGTAAAGAT 2040
Qy 2041 GCGTTCCTTCTCACTGTAATGAATTTGCTTCCCTCATGTGTGAATACACTTTTCCAATAACAGC 2100
Db 2041 GCGTTCCTTCTCACTGTAATGAATTTGCTTCCCTCATGTGTGAATACACTTTTCCAATAACAGC 2100
Qy 2101 ACAGCCTCCAAAGGGAATTTCTGAGGAAGAGACAGTACCTGTGGGAGTCCCTGTG 2160
Db 2101 ACAGCCTCCAAAGGGAATTTCTGAGGAAGAGACAGTACCTGTGGGAGTCCCTGTG 2160
Qy 2161 CAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGCAGGATCACATCCT 2220
Db 2161 CAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGCAGGATCACATCCT 2220
Qy 2221 TTCTTAAAAAGACAAACAGAAAGTGTGTGACCTTGTGTATTTACTATTTACGCGTT 2280
Db 2221 TTCTTAAAAAGACAAACAGAAAGTGTGTGACCTTGTGTATTTACTATTTACGCGTT 2280
Qy 2281 GTTGTTCAGTGGCACATACCTCAACGGGGATATGGAGAGCTATTTCCCAACCTCGCTG 2340
Db 2281 GTTGTTCAGTGGCACATACCTCAACGGGGATATGGAGAGCTATTTCCCAACCTCGCTG 2340
Qy 2341 CTGACCTCATCTGGGGTTTTCTGTAGCTTAAAGCGGTGCAACTGCTTAAAGTGAATTGT 2400
Db 2341 CTGACCTCATCTGGGGTTTTCTGTAGCTTAAAGCGGTGCAACTGCTTAAAGTGAATTGT 2400
Qy 2401 AGAATCAGTAAGGCTGGAAAGACCAAGATCATTAAGTCCAACTGTCAGCCCCATCCCC 2460
Db 2401 AGAATCAGTAAGGCTGGAAAGACCAAGATCATTAAGTCCAACTGTCAGCCCCATCCCC 2460
Qy 2461 ACCGCGCCCATCTGTCACTCAGTGGCCATCCAGCATTTCTTGAACATCTCCAGGACAG 2520
Db 2461 ACCGCGCCCATCTGTCACTCAGTGGCCATCCAGCATTTCTTGAACATCTCCAGGACAG 2520
Qy 2521 TGACTCCACCCGTCACCACTGTGCTTTCAGAGCAGGCGAGGTGACAGTCTCAGTGGCCAGT 2580
Db 2521 TGACTCCACCCGTCACCACTGTGCTTTCAGAGCAGGCGAGGTGACAGTCTCAGTGGCCAGT 2580
Qy 2581 TGATCCTGCTGAAGAGCTTAAACAGTGCAGTTTAAACAAACGAGCTGATTTGTGTGATGGT 2640
Db 2581 TGATCCTGCTGAAGAGCTTAAACAGTGCAGTTTAAACAAACGAGCTGATTTGTGTGATGGT 2640
Qy 2641 TGCTGAATCAGTACGTTGAGATGTCACTAACTTTTGGAGATTAATTTCAGGATGGAAC 2700
Db 2641 TGCTGAATCAGTACGTTGAGATGTCACTAACTTTTGGAGATTAATTTCAGGATGGAAC 2700
Qy 2701 ACATTTCTAACCCCTGAAACAGGCTTTGATTTGGGCTTGGCATTTGCAGAAATTTGCAGGA 2760
Db 2701 ACATTTCTAACCCCTGAAACAGGCTTTGATTTGGGCTTGGCATTTGCAGAAATTTGCAGGA 2760
Qy 2761 AAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAACAGAAATTAACACTTACAC 2820
Db 2761 AAAGATTGTTTGGGAACAGATGAATGGAATTTCCACCAACAGAAATTAACACTTACAC 2820
Qy 2821 CAGTTTGAGTCTGGTCTTGGTTCGATATTTCTTAAAGAAATCTCATCTCCCTGCTCTT 2880
Db 2821 CAGTTTGAGTCTGGTCTTGGTTCGATATTTCTTAAAGAAATCTCATCTCCCTGCTCTT 2880

Qy 2881 GGACCACTGTCTGACAGGAGGTGGAGGATCATCAGGGTTCAGCATCTCCTCAGCATCTAGG 2940
Db 2881 GGACCACTGTCTGACAGGAGGTGGAGGATCATCAGGGTTCAGCATCTCCTCAGCATCTAGG 2940
Qy 2941 GATGTGCACTATGTGTGATGGTGACACTTTAGAGAACTGCTTTGATTTCCCGAGGGCTTTC 3000
Db 2941 GATGTGCACTATGTGTGATGGTGACACTTTAGAGAACTGCTTTGATTTCCCGAGGGCTTTC 3000
Qy 3001 CCTCTCTTCCATCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAACCTTCAGC 3060
Db 3001 CCTCTCTTCCATCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAACCTTCAGC 3060
Qy 3061 ACCGCTCTGCTCTGCTAGGCTTTCATAGAGGCCACAGGGACTGTAGCCAGGCAATGACC 3120
Db 3061 ACCGCTCTGCTCTGCTAGGCTTTCATAGAGGCCACAGGGACTGTAGCCAGGCAATGACC 3120
Qy 3121 TTTTCCAGGCGTCTCTGAATCCAGCACTGTGGTGGGAGGAGCTCTGTGCTCTGGG 3180
Db 3121 TTTTCCAGGCGTCTCTGAATCCAGCACTGTGGTGGGAGGAGCTCTGTGCTCTGGG 3180
Qy 3181 TGCTGAGTGAAGCAGGAAAGCTCAAGCTCAGCTTTTGTTCCTTTAGTGAAGGTTAAATTTCG 3240
Db 3181 TGCTGAGTGAAGCAGGAAAGCTCAAGCTCAGCTTTTGTTCCTTTAGTGAAGGTTAAATTTCG 3240
Qy 3241 AGCTTGGCGTAAATCATAGCTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAAAT 3300
Db 3241 AGCTTGGCGTAAATCATAGCTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAAAT 3300
Qy 3301 CCACAAACATAGCAGCGGAAAGCAATAAGTGAAGCTTGGGCTGCTTAATGAGTGAGC 3360
Db 3301 CCACAAACATAGCAGCGGAAAGCAATAAGTGAAGCTTGGGCTGCTTAATGAGTGAGC 3360
Qy 3361 TAACTCACAATTAATGCGTTTGCCTCACTGCCCGCTTTCAGTCCGGAACCTGCTGCTGC 3420
Db 3361 TAACTCACAATTAATGCGTTTGCCTCACTGCCCGCTTTCAGTCCGGAACCTGCTGCTGC 3420
Qy 3421 CAGCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTTCGCTATTTGGCGCTCT 3480
Db 3421 CAGCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTTCGCTATTTGGCGCTCT 3480
Qy 3481 TCCGCTTCTCGCTCACTGATCGCTGCGCTCGCTTTCGCTGCGGCGAGCGGTATCA 3540
Db 3481 TCCGCTTCTCGCTCACTGATCGCTGCGCTCGCTTTCGCTGCGGCGAGCGGTATCA 3540
Qy 3541 GCTCAGCTCAAAAGCGGTATACCGTTATCCACAGAAATCAGGGGATACCGCAGGAAAGAAC 3600
Db 3541 GCTCAGCTCAAAAGCGGTATACCGTTATCCACAGAAATCAGGGGATACCGCAGGAAAGAAC 3600
Qy 3601 ATGTGAGCAAAAGCGCAGCAAAAGCGCAGGAAACCGTAAAAAGGCGGTTTGTGGCGTTT 3660
Db 3601 ATGTGAGCAAAAGCGCAGCAAAAGCGCAGGAAACCGTAAAAAGGCGGTTTGTGGCGTTT 3660
Qy 3661 TTCCATAGGCTCCGCCCCCTGACAGCATCAAAAAATCGACGCTCAAGTTCAGAGGTGG 3720
Db 3661 TTCCATAGGCTCCGCCCCCTGACAGCATCAAAAAATCGACGCTCAAGTTCAGAGGTGG 3720
Qy 3721 CGAAACCGACAGGACTATTAAGATACCAAGCGGTTTCCCGCTGGAAGCTCCCTGCTGCGC 3780
Db 3721 CGAAACCGACAGGACTATTAAGATACCAAGCGGTTTCCCGCTGGAAGCTCCCTGCTGCGC 3780
Qy 3781 TCTCTCTGTTCCGACCTTGCCTTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGC 3840
Db 3781 TCTCTCTGTTCCGACCTTGCCTTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGC 3840
Qy 3841 GTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTTAGGTGCTTCCGCTCC 3900
Db 3841 GTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTTAGGTGCTTCCGCTCC 3900
Qy 3901 AAGCTGGGCTGTGTGACGAAACCCCGTTTACGCCAGCCGCTGCGCTTATCCGTTAAC 3960
Db 3901 AAGCTGGGCTGTGTGACGAAACCCCGTTTACGCCAGCCGCTGCGCTTATCCGTTAAC 3960

3961 TATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTTGGCAGCAGCACTGGT 4020
|||||
Db
3961 TATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGCGCAGCAGCACTGGT 4020
|||||
Qy
4021 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCGTTGAAGTGGTGCCT 4080
|||||
Db
4021 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCGTTGAAGTGGTGCCT 4080
|||||
Qy
4081 AACTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC 4140
|||||
Db
4081 AACTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC 4140
|||||
Qy
4141 TTCGAAAAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACCAACCGCTGCTAGCGGTGGT 4200
|||||
Db
4141 TTCGAAAAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACCAACCGCTGCTAGCGGTGGT 4200
|||||
Qy
4201 TTTTCTTTTTCGAAAGCAGCAGATTACCGCGCAGAAAAAAGATCTCAAGAAAGATCCCTTTG 4260
|||||
Db
4261 ATCTTTTCTACGGGTCTGAGCTCAGAGAACTCTCGTCAAGAGGCGATAGAGGCGATG 4320
|||||
Qy
4261 ATCTTTTCTACGGGTCTGAGCTCAGAGAACTCTCGTCAAGAGGCGATAGAGGCGATG 4320
|||||
Db
4321 CGCTGCGAATCGGAGCGGCGATACCGTAAAGCAGCAGAGGAGCGGTCAAGCCATTCGCCG 4380
|||||
Qy
4321 CGCTGCGAATCGGAGCGGCGATACCGTAAAGCAGCAGAGGAGCGGTCAAGCCATTCGCCG 4380
|||||
Db
4381 CCAAGCTCTTCAGCAATATCAOGGATAGCCAAACGCTATGCTCTGATAGCGGTCCGCCA 4440
|||||
Qy
4381 CCAAGCTCTTCAGCAATATCAOGGATAGCCAAACGCTATGCTCTGATAGCGGTCCGCCA 4440
|||||
Db
4441 CCCAGCCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATTCGGC 4500
|||||
Qy
4441 CCCAGCCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATTCGGC 4500
|||||
Db
4501 AAGCAGCAGTCGCCATCGGTCACGACGAGATCTCGCGCTCGGCGATGCGCGCTTCGAGC 4560
|||||
Qy
4501 AAGCAGCAGTCGCCATCGGTCACGACGAGATCTCGCGCTCGGCGATGCGCGCTTCGAGC 4560
|||||
Db
4561 CTGCGCAACAGTTCGGCTGCGCGAGCCCTGATGCTCTTCGTCAGATCATCTGATCG 4620
|||||
Qy
4561 CTGCGCAACAGTTCGGCTGCGCGAGCCCTGATGCTCTTCGTCAGATCATCTGATCG 4620
|||||
Db
4621 ACAAGACGGCTTCATCCGAGTACGTCTCGCTCGATGCGATGTTTCGCTTGGTGGTGG 4680
|||||
Qy
4621 ACAAGACGGCTTCATCCGAGTACGTCTCGCTCGATGCGATGTTTCGCTTGGTGGTGG 4680
|||||
Db
4681 AATGGGCAAGGTAGCGGATCAAGCGTATGACGCGCGCGCATTTGATCAGCGCATGATGGAT 4740
|||||
Qy
4681 AATGGGCAAGGTAGCGGATCAAGCGTATGACGCGCGCGCATTTGATCAGCGCATGATGGAT 4740
|||||
Db
4741 ACTTTCTCGGAGGAGCAAGGTAGATGACAGGAGATCTCTGCCCGCACCTTCGCCCAAT 4800
|||||
Qy
4741 ACTTTCTCGGAGGAGCAAGGTAGATGACAGGAGATCTCTGCCCGCACCTTCGCCCAAT 4800
|||||
Db
4801 AGCAGCAGTCCCTTCGCTTTCAGTCAACAGCTGAGCAGCAGCTGCGCAAGGACGCC 4860
|||||
Qy
4801 AGCAGCAGTCCCTTCGCTTTCAGTCAACAGCTGAGCAGCAGCTGCGCAAGGACGCC 4860
|||||
Db
4861 GTGCTGCGCAGCAGCAGTACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4920
|||||
Qy
4861 GTGCTGCGCAGCAGCAGTACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4920
|||||
Db
4921 AGGTGCTGCTTTCGCAAAAAAGAACCGGGCGCCCTTCGCTGATGACCGCGGCAACCGCGCA 4980
|||||
Qy
4921 AGGTGCTGCTTTCGCAAAAAAGAACCGGGCGCCCTTCGCTGATGACCGCGGCAACCGCGCA 4980
|||||
Db
4981 TCAGAGCAGCGGATGCTGTTGTGCGCAGTCATAGCGGATAGCGCTTCACCCAGCG 5040
|||||
Qy
4981 TCAGAGCAGCGGATGCTGTTGTGCGCAGTCATAGCGGATAGCGCTTCACCCAGCG 5040
|||||
Db
5041 GCCGAGAACTCGGTGCAATCCATCTTGTTCATCATCGAAACGATCTCTCATCTCTGTC 5100
|||||

5041 GCCGAGAACTCGGTGCAATCCATCTTGTTCATCATCGAAACGATCTCTCATCTCTGTC 5100
|||||
Db
5101 TCTTGATCAGATCTTGATCCCTTGGCCCATCAGATCTTGGCGGCGAAGAGCCATCCAG 5160
|||||
Qy
5101 TCTTGATCAGATCTTGATCCCTTGGCCCATCAGATCTTGGCGGCGAAGAGCCATCCAG 5160
|||||
Db
5161 TTTTACTTTTGCAGGGCTTCCCAAACCTTACAGAGGGGCCCCAGCTGGCAATTCGGTTCG 5220
|||||
Qy
5161 TTTTACTTTTGCAGGGCTTCCCAAACCTTACAGAGGGGCCCCAGCTGGCAATTCGGTTCG 5220
|||||
Db
5221 CTTTGTCTCCATAAAAAACCGCCCATCTAGCAAATGTTGGAAAGGGCGATCGGTGCGGCC 5280
|||||
Qy
5221 CTTTGTCTCCATAAAAAACCGCCCATCTAGCAAATGTTGGAAAGGGCGATCGGTGCGGCC 5280
|||||
Db
5281 TCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGCTGCAAGGCGATTAAGTTGGGTA 5340
|||||
Qy
5281 TCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGCTGCAAGGCGATTAAGTTGGGTA 5340
|||||
Db
5341 ACGCCAGGGTTTTCCCAAGTCACGACGTTGTAAAAACGACGCCAGTGAATTTGTAATACGAC 5400
|||||
Qy
5341 ACGCCAGGGTTTTCCCAAGTCACGACGTTGTAAAAACGACGCCAGTGAATTTGTAATACGAC 5400
|||||
Db
5401 TCACTATAGGGCGAATTTGGAGCT 5423
|||||
Qy
5401 TCACTATAGGGCGAATTTGGAGCT 5423
|||||
Db
5401 TCACTATAGGGCGAATTTGGAGCT 5423
|||||

RESULT 2
AA88055
ID AA88055 standard; DNA; 5707 BP.
XX
AC AA88055;
XX
DT 08-SEP-1999 (first entry)
XX
DE Plasmid pIG0335 DNA.
XX
KW Plasmid pIG0335; expression vector; treatment; disease;
KW RNA stability element; gene therapy; muscle atrophy; neurological;
KW muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW clotting factor; atherogenesis; atherosclerotic; cardiovascular;
KW cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW diabetes; transgenic animal; carcinogen; regulatory element;
KW livestock improvement; immune response; ds.
XX
OS Synthetic.
XX
PN US5925564-A.
XX
PD 20-JUL-1999.
XX
PF 07-JUN-1995; 95US-00472809.
XX
PR 06-NOV-1991; 91US-00789919.
XX
PR 09-MAR-1994; 94US-00209846.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI O'malley BW, Demayo FJ, Schwartz RJ;
XX
DR WPI; 1999-418276/35.
XX
PT New expression vector system useful for gene therapy.
XX
PS Disclosure; Fig 17-17F; 67pp; English.
XX
CC This invention describes novel expression vector systems containing RNA
CC stability elements from 3' flanking sequences used for establishing
CC expression of a nucleic acid sequence within a tissue. The vectors also
CC facilitate enhanced expression in tissues and target expression with
CC tissue specificity. The expression vectors can be used to treat diseases
CC through gene therapy by targeting the vector to specific tissues.

Db 2447 CACATCCCTTTCTTAAAGACAAACAGAGGTAGTGTGACCTTGTGTAATTAATAAT 2506
Qy 2273 TAGCGTGTGTTCTCAGTGSCATATCCTCAACGGGGATATGAGAGCTAATTTCCCAAC 2332
Db 2507 TAGCGGTGTGTTCAGTGSCATATCCTCAACGGGGATATGAGAGCTAATTTCCCAAC 2566
Qy 2333 CCTCGCTGTGGACCCCTGATCTGGGGTTTTCTGTAGCTTTAAGCGGTGCCAACTGCTTAA 2392
Db 2567 CCTCGCTGTGGACCCCTGATCTGGGGTTTTCTGTAGCTTTAAGCGGTGCCAACTGCTTAA 2626
Qy 2393 GTGATGTAGAAATCAGTAAGCTTGGAAAGACACACAGATCATTAAGTCCAACTGTAGCC 2452
Db 2627 GTGATGTAGAAATCAGTAAGCTTGGAAAGACACACAGATCATTAAGTCCAACTGTAGCC 2686
Qy 2453 CCATCCCAACGGGCCCACTGTCACTCAGTGCCACATCCACGATTTCTTGACATCTCC 2512
Db 2687 CCATCCCAACGGGCCCACTGTCACTCAGTGCCACATCCACGATTTCTTGACATCTCC 2746
Qy 2513 AGGACACAGTGACTCCACCCGTCAACAGCTGTGCTTCAAGCAGGCGAGGTGACAGTCTCA 2572
Db 2747 AGGACACAGTGACTCCACCCGTCAACAGCTGTGCTTCAAGCAGGCGAGGTGACAGTCTCA 2806
Qy 2573 GTGCCAGTTGCATCTCTCTGAAGAGCTTAAACAGTGCAGTTTAAACAAACGGACTGATTTGTT 2632
Db 2807 GTGCCAGTTGCATCTCTCTGAAGAGCTTAAACAGTGCAGTTTAAACAAACGGACTGATTTGTT 2866
Qy 2633 GATGTGTTGCTGATCAGTACGTTAGATGTCTAAACCTTTTGGAGATTAATTTTCA 2692
Db 2867 GATGTGTTGCTGATCAGTACGTTAGATGTCTAAACCTTTTGGAGATTAATTTTCA 2926
Qy 2693 GATGGAACACATTTCTTAACCTGAAACAGCCTTTGATTTGGGCTGGCATTTGCGAAT 2752
Db 2927 GATGGAACACATTTCTTAACCTGAAACAGCCTTTGATTTGGGCTGGCATTTGCGAAT 2986
Qy 2753 TTGCAGGAAAGATGTTTGGGAACAGATGAATGGAAATTTCCACAAACAGAAATTAAC 2812
Db 2987 TTGCAGGAAAGATGTTTGGGAACAGATGAATGGAAATTTCCACAAACAGAAATTAAC 3046
Qy 2813 ACTTACACAGTTTGAGTCTGGTCTTCGTTGATTAATTTCTTAAGAAATCTCATCTCTCC 2872
Db 3047 ACTTACACAGTTTGAGTCTGGTCTTCGTTGATTAATTTCTTAAGAAATCTCATCTCTCC 3106
Qy 2873 CTGCTCTTTGACACAGTCTGCTGACAGAGGTGAGGATCATCAGGGTCAAGCATCTCTCAG 2932
Db 3107 CTGCTCTTTGACACAGTCTGCTGACAGAGGTGAGGATCATCAGGGTCAAGCATCTCTCAG 3166
Qy 2933 CATCTAGGGATGTGCACTATGTGTGATGGTGACATTTTAGAGAACTGCTTTTGAATCCCCA 2992
Db 3167 CATCTAGGGATGTGCACTATGTGTGATGGTGACATTTTAGAGAACTGCTTTTGAATCCCCA 3226
Qy 2993 GGGCTTTCCCTCTCTTCATGTCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTCTGAA 3052
Db 3227 GGGCTTTCCCTCTCTTCATGTCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTCTGAA 3286
Qy 3053 CTTCACAGCCGTCTGCTCTGCTGAGGTGTTCCATAGAGCCACAGGGCTGTGAGCCAG 3112
Db 3287 CTTCACAGCCGTCTGCTCTGCTGAGGTGTTCCATAGAGCCACAGGGCTGTGAGCCAG 3346
Qy 3113 GCATGACCTTTTCCAGCCGTCTCTGAATCCAGCACTGTGGTGGGAGGCACTCTGG 3172
Db 3347 GCATGACCTTTTCCAGCCGTCTCTGAATCCAGCACTGTGGTGGGAGGCACTCTGG 3406
Qy 3173 TCCTGGGGTGTGAGTGAGCCAGGGAACAAGCT----- 3206
Db 3407 TCCTGGGGTGTGAGTGAGCCAGGGAACAAGCTTATCGATACCGTCCGACCTCGAGGGGG 3466
Qy 3207 -----CAGCTTTGTTCCCTTTAGTGAGGGTTAATTTTCAGCTTTGGGCTAATCA 3255
Db 3467 GGCCCGGTACCCAGCTTTGTTTCCCTTTAGTGAGGGTTAATTTTCAGCTTTGGGCTAATCA 3526
Qy 3256 TGGTCATAGCTGTTTCTCTGTGAAATTTGTTATCCGCTCACAATTTCCACAAACATACGA 3315
Db 3527 TGGTCATAGCTGTTTCTCTGTGAAATTTGTTATCCGCTCACAATTTCCACAAACATACGA 3586

Qy 3316 GCGGAAGCATAAAGTGTAAAGCTCGGGTGCCTAATGAGTGAAGTAACTCACATTAATTT 3375
Db 3587 GCGGAAGCATAAAGTGTAAAGCTCGGGTGCCTAATGAGTGAAGTAACTCACATTAATTT 3646
Qy 3376 GCGTTGCGCTCACTGCGCCGCTTTCCAGTCGGGAAACCTGTCGTGCAGCTGCAATTAATGA 3435
Db 3647 GCGTTGCGCTCACTGCGCCGCTTTCCAGTCGGGAAACCTGTCGTGCAGCTGCAATTAATGA 3706
Qy 3436 ATCGGCCAACGGCGGGGAGAGCGGTTTGGGTAATTTGGGGCTCTTCCGCTTCTCGCTC 3495
Db 3707 ATCGGCCAACGGCGGGGAGAGCGGTTTGGGTAATTTGGGGCTCTTCCGCTTCTCGCTC 3766
Qy 3496 ACTGACTCTCGTGGCTCGGTTCGGCTGCGCGAGCGGTATCAGTCACTCAAAAGGCG 3555
Db 3767 ACTGACTCTCGTGGCTCGGTTCGGCTGCGCGAGCGGTATCAGTCACTCAAAAGGCG 3826
Qy 3556 GTAAATACGGTTATCCACAGAAATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGC 3615
Db 3827 GTAAATACGGTTATCCACAGAAATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGC 3886
Qy 3616 CAGCAAAAGCCAGGAACCGTAAAGGCGCGTTCGTGGCGTTTTCATAGGCTCCGC 3675
Db 3887 CAGCAAAAGCCAGGAACCGTAAAGGCGCGTTCGTGGCGTTTTCATAGGCTCCGC 3946
Qy 3676 CCCCTGACGAGCATCACAAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGA 3735
Db 3947 CCCCTGACGAGCATCACAAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGA 4006
Qy 3736 CTATAAGATACACAGCGGTTTCCCTGGAAGCTCCCTGTCGCTCTCTCTGTTCGAGCC 3795
Db 4007 CTATAAGATACACAGCGGTTTCCCTGGAAGCTCCCTGTCGCTCTCTCTGTTCGAGCC 4066
Qy 3796 CTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAT 3855
Db 4067 CTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAT 4126
Qy 3856 AGCTCAGCTGTAGGTATCTCAGTTCGCTGTAGGTCTCGCTCCAAGCTGGGCTGTGTG 3915
Db 4127 AGCTCAGCTGTAGGTATCTCAGTTCGCTGTAGGTCTCGCTCCAAGCTGGGCTGTGTG 4186
Qy 3916 CACGAACCCCGCTTACAGCCCGCTGCGCTTATTCGGTAACTATATCGTCTGTAGTCC 3975
Db 4187 CACGAACCCCGCTTACAGCCCGCTGCGCTTATTCGGTAACTATATCGTCTGTAGTCC 4246
Qy 3976 AACCCGGTAAGACACAGACTTATCGCCACTGCGCAGCCACTGGTAACAGGATTAGCAGA 4035
Db 4247 AACCCGGTAAGACACAGACTTATCGCCACTGCGCAGCCACTGGTAACAGGATTAGCAGA 4306
Qy 4036 GCGAGGTATCTAGCGGTGCTACAGAGTTCCTGAAAGTGGTGGCTAACTACGGCTACACT 4095
Db 4307 GCGAGGTATCTAGCGGTGCTACAGAGTTCCTGAAAGTGGTGGCTAACTACGGCTACACT 4366
Qy 4096 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCAGTTACCTTCGGAAGAGGTT 4155
Db 4367 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCAGTTACCTTCGGAAGAGGTT 4426
Qy 4156 GGTAGCTCTTGATTCGGCAAAACAAACCAACCGCTGAGCGGTGTTTTTTTGTTCGCAAG 4215
Db 4427 GGTAGCTCTTGATTCGGCAAAACAAACCAACCGCTGAGCGGTGTTTTTTTGTTCGCAAG 4486
Qy 4216 CAGCAGATTAACGCGCAAAAGAAAGGATCTCAAGAGATCTTTTGAATCTTTTCTACGGGG 4275
Db 4487 CAGCAGATTAACGCGCAAAAGAAAGGATCTCAAGAGATCTTTTGAATCTTTTCTACGGGG 4546
Qy 4276 TCTGACGCTCAGAAAGAACTCTGTCGAAGAGCGATAGAGCGGATGCGCTCGGAATCGGGA 4335
Db 4547 TCTGACGCTCAGAAAGAACTCTGTCGAAGAGCGATAGAGCGGATGCGCTCGGAATCGGGA 4606
Qy 4336 GCGCGATACCGTAAGACACAGAGAGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCA 4395
Db 4607 GCGCGATACCGTAAGACACAGAGAGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCA 4666

QY 4396 ATATCATCGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAGCCGGCCACAG 4455
DB |||||
QY 4667 ATATCAGGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAGCCGGCCACAG 4726
DB |||||
QY 4456 TCGATGAATCCAGAAAGCGGCATTTTCCACCATGATATTCGGCAGCAGGCGATCGCCA 4515
DB |||||
QY 4727 TCGATGAATCCAGAAAGCGGCATTTTCCACCATGATATTCGGCAGCAGGCGATCGCCA 4786
DB |||||
QY 4516 TGGGTCAACGACGAGATCTCTCGCGTGGGCGATCGCGCCCTTGAGCCTTGGCGAACAAGTTGG 4575
DB |||||
QY 4787 TGGGTCAACGACGAGATCTCTCGCGTGGGCGATCGCGCCCTTGAGCCTTGGCGAACAAGTTGG 4846
DB |||||
QY 4576 GCTGGCGCGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAAGCCGGCTTCC 4635
DB |||||
QY 4847 GCTGGCGCGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAAGCCGGCTTCC 4906
DB |||||
QY 4636 ATCCGAGTAGTCTCTCGCTCGATGCGATGTTTCTGCTTGGTGGTCCGAATGGGCGAGTAGCC 4695
DB |||||
QY 4907 ATCCGAGTAGTCTCTCGCTCGATGCGATGTTTCTGCTTGGTGGTCCGAATGGGCGAGTAGCC 4966
DB |||||
QY 4696 GGATCAAGCGTATGACGCGCCCGCATTTGCAATCAGCCATGATGATATCTTTCTCGCAGGA 4755
DB |||||
QY 4967 GGATCAAGCGTATGACGCGCCCGCATTTGCAATCAGCCATGATGATATCTTTCTCGCAGGA 5026
DB |||||
QY 4756 GCAAGGTGATGACAGGAGATCTCTGCGCCCGGCATTTGGCCCAATAGCAGCCAGTCCCTT 4815
DB |||||
QY 5027 GCAAGGTGATGACAGGAGATCTCTGCGCCCGGCATTTGGCCCAATAGCAGCCAGTCCCTT 5086
DB |||||
QY 4816 CCGCTTTCAGTGAACAGCTCGACAGCTGCGCAAGGACGCCCTGCTGGCGACGCCAC 4875
DB |||||
QY 5087 CCGCTTTCAGTGAACAGCTCGACAGCTGCGCAAGGACGCCCTGCTGGCGACGCCAC 5146
DB |||||
QY 4876 GATAGCGCGCTGCTCTGCTCTGCTCACTTCAATCAGGCGCACCGGACAGGTCTGTTGACA 4935
DB |||||
QY 5147 GATAGCGCGCTGCTCTGCTCTGCTCACTTCAATCAGGCGCACCGGACAGGTCTGTTGACA 5206
DB |||||
QY 4936 AAAAGAACCGGGCGCCCTCGCTGCTGACAGCGGAAACCGCGGCATCAGAGCAGCCGAT 4995
DB |||||
QY 5207 AAAAGAACCGGGCGCCCTCGCTGCTGACAGCGGAAACCGCGGCATCAGAGCAGCCGAT 5266
DB |||||
QY 4996 GTCTGTGTGCCAGTCATAGCCGATAGCTTCCACCCAGCGCGCCGAGAACCTGG 5055
DB |||||
QY 5267 GTCTGTGTGCCAGTCATAGCCGATAGCTTCCACCCAGCGCGCCGAGAACCTGG 5326
DB |||||
QY 5056 TGCATATCCATCTGTTCATATGCGAAACGATCTCTCATCTCTCTCTTCTGATCAGATCTT 5115
DB |||||
QY 5327 TGCATATCCATCTGTTCATATGCGAAACGATCTCTCATCTCTCTCTTCTGATCAGATCTT 5386
DB |||||
QY 5116 GATCCCTTGGCCATCAGATCTCTTGGCGCAAGAAAGCCATCCAGTTTACTTTGCAAGGCG 5175
DB |||||
QY 5387 GATCCCTTGGCCATCAGATCTCTTGGCGCAAGAAAGCCATCCAGTTTACTTTGCAAGGCG 5446
DB |||||
QY 5176 TTCCCAACCTTACAGAGGCGCCCGCAGCTGGCAATTCGGTTTGGTCTGCTGTTCATATAA 5235
DB |||||
QY 5447 TTCCCAACCTTACAGAGGCGCCCGCAGCTGGCAATTCGGTTTGGTCTGCTGTTCATATAA 5506
DB |||||
QY 5236 ACCGCCAGCTAGCAACTGTTGGGAAGGCGCGATCGTGGGCGCTCTTGGCTATTACCG 5295
DB |||||
QY 5507 ACCGCCAGCTAGCAACTGTTGGGAAGGCGCGATCGTGGGCGCTCTTGGCTATTACCG 5566
DB |||||
QY 5296 CAGCTGGCGAAAGGGGATGTGCTGCAAGGCGGATTAAGTTGGGTACGCGAGGTTTTC 5355
DB |||||
QY 5567 CAGCTGGCGAAAGGGGATGTGCTGCAAGGCGGATTAAGTTGGGTACGCGAGGTTTTC 5626
DB |||||
QY 5356 CAGTCAAGCGTTGTAAGAACGAGCGGCAGTGAATTTGTAATGACATCACTATAGGGCGAA 5415
DB |||||
QY 5627 CAGTCAAGCGTTGTAAGAACGAGCGGCAGTGAATTTGTAATGACATCACTATAGGGCGAA 5686
DB |||||
QY 5416 TTGGAGCT 5423
DB |||||
QY 5687 TTGGAGCT 5694
DB |||||

RESULT 3

AAx8054
ID AAX8054 standard; DNA; 6345 BP.
XX
AC AAX8054;
XX
XX 08-SEP-1999 (first entry)
DT
XX Plasmid pIG0100A DNA.
DE
XX Plasmid pIG0100A; plasmid pIG0335; expression vector; treatment; disease;
KW RNA stability element; gene therapy; muscle atrophy; neurological;
KW muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW clotting factor; atherogenesis; atherosclerotic; cardiovascular;
KW cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW diabetes; transgenic animal; carcinogen; regulatory element;
KW livestock improvement; immune response; ds.
XX
OS Synthetic.
XX
PN US5925564-A.
XX
PD 20-JUL-1999.
XX
PF 07-JUN-1995; 95US-00472809.
XX
PR 06-NOV-1991; 91US-00789919.
PR 09-MAR-1994; 94US-00209846.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI O'malley BW, Demayo FJ, Schwartz RJ;
XX WPI; 1999-418276/35.
XX
PT New expression vector system useful for gene therapy.
XX
PS Disclosure; Fig 15-15G; 67pp; English.
XX
CC This invention describes novel expression vector systems containing RNA
CC stability elements from 3' flanking sequences used for establishing
CC expression of a nucleic acid sequence within a tissue. The vectors also
CC facilitate enhanced expression in tissues and target expression with
CC tissue specificity. The expression vectors can be used to treat diseases
CC through gene therapy by targeting the vector to specific tissues.
CC Diseases that can be treated include muscle atrophy associated with
CC neurological, muscular or systemic disease, aging by causing tissues to
CC express trophic factors, haemophilia by causing tissues to express and
CC secrete clotting factor into the circulation, atherogenesis and
CC atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular
CC disease by causing tissues to express factors involved in tissue
CC metabolism. They can be used to replace genes of inherited genetic
CC defects or acquired hormone deficiencies e.g. diabetes. To transform
CC cells to produce particular proteins or RNA in vitro. To create
CC transgenic animals which can be used for research into human diseases,
CC assessing novel therapeutic methods, assessing the effect of chemical and
CC physical carcinogens and for studying the effect of genes and genetic
CC regulatory elements on livestock improvement. They can be used to induce
CC an immune response. These vectors provide controlled expression of the
CC genes they carry and produce a significantly high level of expression.
CC Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the
CC vectors which causes increased expression
XX
SQ Sequence 6345 BP; 1453 A; 1702 C; 1689 G; 1501 T; 0 U; 0 Other;

Query Match 51.4%; Score 2785.8; DB 2; Length 6345;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2787; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 413 CCATGGGAAAAATCAGCAGTCTTCCAAACCAATATTATTAAGTCTGCTTTGTGATTCT 472
DB |||||
3556 CCATGGGAAAAATCAGCAGTCTTCCAAACCAATATTATTAAGTCTGCTTTGTGATTCT 3615

5776	Db	GATGTGGTGTCTGAAATCAGTACGTTTGAGATGTCACTAAACTTTTGGAGATTAAATTTTCAG	5835
2693	Qy	GATGGAAACACATCTTAAACCCCTGAACCAGCCTTTTGATTTTGGGCTTGGCATTTTGCAGAAT	2752
5836	Db	GATGGAAACACATCTTAAACCCCTGAACCAGCCTTTTGATTTTGGGCTTGGCATTTTGCAGAAT	5895
2753	Qy	TTGCAGGAAAAGATTGTTTGGGAAACAGATGAATGGAAATTTCCACCAACACAGAAAAATTAAAC	2812
5896	Db	TTGCAGGAAAAGATTGTTTGGGAAACAGATGAATGGAAATTTCCACCAACACAGAAAAATTAAAC	5955
2813	Qy	ACTTATACACCAAGTTTGAAGTCTGCTCTCGTTCGATATTTCTTAAGAATCTCATCATCTCTCC	2872
5956	Db	ACTTATACACCAAGTTTGAAGTCTGCTCTCGTTCGATATTTCTTAAGAATCTCATCATCTCTCC	6015
2873	Qy	CTGCTCTTTGGACCAAGTCTGCTGACAGGAGGTGAGGATCATCAGGGCTCAGCATCTCTTCAG	2932
6016	Db	CTGCTCTTTGGACCAAGTCTGCTGACAGGAGGTGAGGATCATCAGGGCTCAGCATCTCTTCAG	6075
2933	Qy	CATCTAGGGATGTGCATATGTGTGATGGTGACACTTTTAGAGAACTCTCTTTGATTTCCCCA	2992
6076	Db	CATCTAGGGATGTGCATATGTGTGATGGTGACACTTTTAGAGAACTCTCTTTGATTTCCCCA	6135
2993	Qy	GGGCTTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA	3052
6136	Db	GGGCTTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA	6195
3053	Qy	CTTCCAGCACCGTCTGCTCTCTGTTAGGCTGTTCATAGAGGCCACACAGGACTGTAGCCAG	3112
6196	Db	CTTCCAGCACCGTCTGCTCTCTGTTAGGCTGTTCATAGAGGCCACACAGGACTGTAGCCAG	6255
3113	Qy	GCATGACCTTTTCCCAGCCGTGCTCTGAAATCCAGCATCTGTTGGCTGGAGGCGCAGCTCTGG	3172
6256	Db	GCATGACCTTTTCCCAGCCGTGCTCTGAAATCCAGCATCTGTTGGCTGGAGGCGCAGCTCTGG	6315
3173	Qy	TCCTGGGGTGTCTGACGTGAGCCAGGGAAACA	3202
6316	Db	TCCTGGGGTGTCTGACGTGAGCCAGGGAAACA	6345

RESULT 4

ADS73977
ID ADS73977 standard; DNA; 2237 BP.

XX

AC ADS73977;

XX
DT 16-DEC-2004 (F: rgt cntm.)

DI 18-DEC-2004 (L118C empty) XX

DE Skeletal alpha-actin 3'-end nucleotide fragment.
XX
KW IGF-1; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
KW TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
KW vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
KW cardiant; vasotrophic; ophthalmological; cerebroprotective; ds.
KW

XX

OS Synthetic.

XX
BN
W03004081040-12

FN NO2004081040-A2.
XX

PD 23-SEP-2004.

XX

PF 11-MAR-2004; 2004WO-US007295.

XX
PR 12-MAR-2003. 2003US-

12-NEW-2003; 200303-0434079E;
FR XX

PA (ADVI-) ADVISYS INC.

for treating diabetes, ischemic heart and cerebrovascular disease.

Claim 6; SEQ ID NO 5; 104pp; English.

The invention relates to an isolated nucleic acid expression construct comprising a myogenic promoter, a nucleic acid sequence encoding an insulin-like growth factor I (IGF-I) or its functional biological equivalent, and a 3' untranslated region (3'UTR), which has in vivo expression activity for the encoded IGF-I in a tissue. The myogenic promoter in the isolated nucleic acid expression construct comprises a transcriptional loci from a family of MEF-1, MEF-2, TGF-1, SRE or SP. The 3'UTR is from a skeletal alpha actin gene or from a human growth hormone. The expression construct further comprises transfection-facilitating vector system that is a plasmid, a viral vector, a liposome, or a cationic lipid. The isolated nucleic acid expression construct also comprises a transfection-facilitating polypeptide having a charged polypeptide and/or poly-L-glutamate. The construct is useful in a method for stimulating angiogenesis, or stimulating myogenesis, or elevating levels of an angiogenic factor, or stimulating endogenous production of an angiopoietin, or treating a muscular or vascular complications of diabetes in a subject. The angiogenic factor comprises a vascular endothelial growth factor (VEGF) or VEGF receptor. The methods and compositions of the present invention are useful for the prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the IGF-I, such as diabetes mellitus, ischaemic heart disease, diabetic retinopathy and cerebrovascular disease. The present sequence represents the nucleotide sequence of a skeletal alpha-actin 3'-end fragment, a specific example of the 3'-UTR fragment used in the nucleic acid expression construct of the invention.

Sequence 2237 BP; 514 A; 567 C; 569 G; 587 T; 0 U; 0 Other;

very Match 41.3%; Score 2237; DB 13; Length 2237;

Local Similarity 100.0%; Pred. No. 1.5e-278;

934 GGAATTCGATGGCCCATCCATTGTCCACCGTAATGCTTCTAAACATGTTACATGATCA 993

A vertical ruler with markings from 0 to 10 cm. The markings are in millimeters, with numbers every centimeter. The ruler is oriented vertically, with the 0 mark at the top and the 10 cm mark at the bottom.

994 CTTTGCCAAACCACTCAGGATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCAC 1053

A

1054 CACCCATGCAACCTTTCCTAATTTTCCTAACAATTCCTGCAACGCTCCTTC 1113

1054 CAGCCAGCAGACCTTCTAATTTGGTAACAAATTCGGTACCTGCTGCAAGCTCCATGTT

1 4 4 1

II14 TGACACAGGTA'GTAAAGTGTACATAAATTAATTACTCGTTTGTTGGTTT II

1174 TAAACCAATGCCCTGTGGAAGGAAACATAAACTTCAAGAAGCATTAAATCATCAGTCA 12

[illegible]

1234 TTCTGTCACACCCCTAATGCAGTTGTTCTGTGCATCATTTCCCTGGGCTCTTCCATCTCT 12

50T YTCIGTACACCCCTAAATGCAGTTGTATTCTGTGATCATTTTCCCTGGGCTCTTCCATCCTT 300

1294 CGCTGACCTGGGACTGGGTGCTGGGGCTGGAGCAGGGGTGGGGCTCTCCAGGGAGAGA 13

361 CGCTGACCTGGGACCTGGGTGCTGGGGCTGGGAGCAGGGGTCTCCAGGGAGAGA 420

1354 TGGCATGGGGAGAGTGATGGGATACTGCTGGGGGGGGGGGACTCACCTGCTGTGGGCTG 14

421 TGGCATGGGAGAGTGGATGGGACTGCTGGGGGGGGGACTACCCCTGCTGTGGGCTG 480

1414 CAGGAAGCCCATTTGGTGACAGAGAGCAGCCCTGGGATGCCCATGACACGGGCAAGCCACTGCA 1415

481 CAGGAAGCCCATTTGGTGCAGAGAGCAGCCTGGGATGCCCATGACAGGGCACCCACTGCA 540

541	Db	 CCGTGTTTCTCCCATGCCCCAGTAGTAGGGAAGGGTTTACGAGCGCGTTTCATTTCTCAGCTGTG	600
1534	QY	GAAGGATTTTGTGTTGGGCTCAGCCTGCCAGAGCAGTAGTACCAGGCAATGCTGTGTCAGCTCCG	1593
601	Db	GAAGGATTTTGTGTTGGGCTCAGCCTGCCAGAGCAGTAGTACCAGGCAATGCTGTGTCAGCTCCG	660
1594	QY	AGCTGTGATGGACAGAGCAAGGCTGCAGCTGAGGCCAGCTGGTGGGCAACAGGTTAAATTT	1653
661	Db	AGCTGTGATGGACAGAGCAAGGCTGCAGCTGAGGCCAGTGGTGGGCAACAGGTTAAATTT	720
1654	QY	AAGAGCTTTTCCACTTATATGGAAGCCCTCCTGCACTCAACCTGTTCCTGGGGCTGG	1713
721	Db	AAGAGCTTTTCCACTTATGGAAGCCCTCCTGCACTCAACCTGTTCCTGGGGCTGG	780
1714	QY	GGGCAGCCAGGGCCACTTCTCAACCCACTGTGACACACAGAGGCTTTGGCTGACACGCCAG	1773
781	Db	GGGCAGCCAGGGCCACTTCTCAACCCACTGTGACACACAGAGGCTTTGGCTGACACGCCAG	840
1774	QY	GACCTCTGTGGCCACAGACTCTTATAGATTTGCTGTGCCCTAGGAGACACAGGGGGCTTT	1833
841	Db	GACCTCTGTGGCCACAGACTCTTATAGATTTGCTGTGCCCTAGGAGACACAGGGGGCTTT	900
1834	QY	CCCTGCCCTGGCTTCTGGCCCCGGCGACATGACAGGAGCTGCCCTATCTGCCCTCTCTTA	1893
901	Db	CCCTGCCCTGGCTTCTGGCCCCGGCGACATGACAGGAGCTGCCCTATCTGCCCTCTCTTA	960
1894	QY	GATGGTCTGGCAGGAAGGCTGCACITGGCTTGGGGCTGATCCATATATACACTGCGAGTA	1953
961	Db	GATGGTCTGGCAGGAAGGCTGCACITGGCTTGGGGCTGATCCATATATACACTGCGAGTA	1020
1954	QY	GGGACAGCACTGCTGGGAAGAAAGATATTTTCAACTGAACTTACTATCAGGCAAGTTA	2013
1021	Db	GGGACAGCACTGCTGGGAAGAAAGATATTTTCAACTGAACTTACTATCAGGCAAGTTA	1080
2014	QY	TTGCTTTATTTGTGATGGTGTAAAGTGGCTTCTTCTCACTGTAATGATTTTGGCCCTCA	2073
1081	Db	TTGCTTTATTTGTGATGGTGTAAAGTGGCTTCTTCTCACTGTAATGATTTTGGCCCTCA	1140
2074	QY	TGTTGTAATACACTTTCCATTAACAGACACAGCCCTCCAAAGGGAATTTCTCGAGGAAGA	2133
1141	Db	TGTTGTAATACACTTTCCATTAACAGACACAGCCCTCCAAAGGGAATTTCTCGAGGAAGA	1200
2134	QY	CAGTACCTGGTGTGGGAAGTCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGA	2193
1201	Db	CAGTACCTGGTGTGGGAAGTCCCTGTGCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGA	1260
2194	QY	CTGGCTGGGAGCAGGAGTACATCCTTTCTTAAAAAGACAAACAGAAAGTGTGTGTGA	2253
1261	Db	CTGGCTGGGAGCAGGAGTACATCCTTTCTTAAAAAGACAAACAGAAAGTGTGTGTGA	1320
2254	QY	CCTTGTCTGTAATTTACTATTTACGGTTGTGTTTCAGTGGGCACATACCTCAACGGGGATAT	2313
1321	Db	CCTTGTCTGTAATTTACTATTTACGGGTTGTGTTTCAGTGGGCACATACCTCAACGGGGATAT	1380
2314	QY	GGAGAGCTATTTCCCAACCTCGCTGTGAGCCCTGATCTGGGGTTTTTCTGTGAGCTTA	2373
1381	Db	GGAGAGCTATTTCCCAACCTCGCTGTGAGCCCTGATCTGGGGTTTTTCTGTGAGCTTA	1440
2374	QY	AGCGGTGCCAACTGCTTAAGTGTATGAAATCAGTAAGGCTGGAAAGACCACAGATCA	2433
1441	Db	AGCGGTGCCAACTGCTTAAGTGTATGAAATCAGTAAGGCTGGAAAGACCACAGATCA	1500
2434	QY	TTAAGTCCAACTGTGAGCCCATCCCAACCGGGCCCATCTGTCACTCAGTGGCCACATCCAC	2493
1501	Db	TTAAGTCCAACTGTGAGCCCATCCCAACCGGGCCCATCTGTCACTCAGTGGCCACATCCAC	1560
2494	QY	GCAATTTCTTGAACATCTCCAGGACAGTGAATCCACCGTCCACAGCTGTGCTTCAGAGC	2553
1561	Db	GCAATTTCTTGAACATCTCCAGGACAGTGAATCCACCGTCCACAGCTGTGCTTCAGAGC	1620
2554	QY	AGGCAGGGTGAAGCTCTCAGTGGCCAGTTGCAATCTCTGTGTGAAGAGCTTAACAGTGCAGTTT	2613

Db	1621	AGGCAGGGTGACAGTCTCAGTGCAGCTTGATCCTCTGCTGAAGAGCTTAAACAGTGCAGTTT	1680
Qy	2614	AACAACGGACTGATTTTGTTCGATGTGGTTGCTGAATCAGTACGTTGAGATCTCACTAAACT	2673
Db	1681	AACACGGACTGATTTGTTGATGTGGTTGCTGAATCAGTACGTTGAGATCTCACTAAACT	1740
Qy	2674	TTTTGGAGATTAAATTCAGGATGGAAACACATCTCTTAAACCTGAAACACAGCCTTTGATTG	2733
Db	1741	TTTTGGAGATTAAATTCAGGATGGAAACACATCTCTTAAACCTGAAACACAGCCTTTGATTG	1800
Qy	2734	GGCTTGGCATTTTCAGGAAATTTGCAGGAAGAATTTGTTGGGAACAGATGAATGGAAATTC	2793
Db	1801	GGCTTGGCATTTTCAGGAAATTTGCAGGAAGAATTTGTTGGGAACAGATGAATGGAAATTC	1860
Qy	2794	CACCAACAGAAATTAACACTTACACAGCTTTTGAGTCTGGTCTTCCGTTGATATTTCTT	2853
Db	1861	CACCAACAGAAATTAACACTTACACAGCTTTTGAGTCTGGTCTTCCGTTGATATTTCTT	1920
Qy	2854	AAGAATCTCATCATCTCCCTGCTCTTTGGACCAAGTGTCTGTACAGAGGTGGAGGATCA	2913
Db	1921	AAGAATCTCATCATCTCCCTGCTCTTTGGACCAAGTGTCTGTACAGAGGTGGAGGATCA	1980
Qy	2914	TCAGGGTCAGCATCTCAGCATCTAGGGATGTGCACATATCTGTGATGGTGACACTTTTGA	2973
Db	1981	TCAGGGTCAGCATCTCAGCATCTAGGGATGTGCACATATCTGTGATGGTGACACTTTTGA	2040
Qy	2974	GAACCTGCTTTGATTCGCCAGGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCT	3033
Db	2041	GAACCTGCTTTGATTCGCCAGGGCTTTCCCTCTCTTCCATGCAGGGCTCACTATCAGCCCT	2100
Qy	3034	GAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGTCTCCTGGTAGGCTGTTCATAGAGG	3093
Db	2101	GAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGTCTCCTGGTAGGCTGTTCATAGAGG	2160
Qy	3094	CCACAGGAGCTGTAGCCAGGATGACCTTTTCCAGCCGTGCTCTGAATCCAGCACTGGT	3153
Db	2161	CCACAGGAGCTGTAGCCAGGATGACCTTTTCCAGCCGTGCTCTGAATCCAGCACTGGT	2220
Qy	3154	GGCTGGGAGCAGCTCT 3170	
Db	2221	GGCTGGGAGCAGCTCT 2237	
RESULT 5			
ID	AAV50428 standard; DNA; 3599 BP.		
XX	AAV50428;		
XX			
DT	26-OCT-1998 (first entry)		
DE	Plasmid pIG0552 lower sequence nucleotides 1-3599.		
XX			
KW	Human; IGF-1; insulin-like growth factor 1; urinary incontinence;		
KW	gene therapy; neurotrophic factor; ss.		
XX			
OS	Synthetic.		
OS	Homo sapiens.		
XX			
PN	W09833529-A1.		
XX			
PD	06-AUG-1998.		
XX			
PF	04-FEB-1998; 98WO-US002051.		
XX			
PR	04-FEB-1997; 97US-0036862P.		
XX			
PA	(GENE-) GENEMEDICINE INC.		
XX			
PI	Coleman M;		
XX			
DR	WPI; 1998-437184/37.		
XX			

PT Treatment of urinary incontinence - by delivering nucleic acid vector for
XX expression of growth factor or neurotrophic factor in tissue(s).

XX Disclosure; Page 105-107; 117pp; English.

XX A method has been developed of treating urinary incontinence (UI) in
CC mammals. The method comprises delivering a nucleic acid vector for the
CC expression of a growth factor or neurotrophic factor in a tissue or
CC tissues. The present sequence represents the actual lower sequence of
CC plasmid pIG0552 nucleotides 1-3599 from the present invention. Due to the
CC growth and stimulatory effects of growth factors and neurotrophic
CC factors, introducing these factors to degenerated muscles in the urinary
CC system can improve UI by enhancing both their integrity and neural
XX innervation

SQ Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 U; 0 Other;
Query Match 40.9%; Score 2218; DB 2; Length 3599;
Best Local Similarity 99.6%; Pred. No. 3.7e-276; Mismatches 10; Indels 0; Gaps 0;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	3190	GAGCCAGGGAACAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG	3249
DB	3	GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG	62
QY	3250	TAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCAAAATTCACACAAC	3309
DB	63	TAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCAAAATTCACACAAC	122
QY	3310	ATAGGAGCCGGAACATAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTAACTACA	3369
DB	123	ATAGGAGCCGGAACATAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTAACTACA	182
QY	3370	TTAATTCGGTTGGCTCAGCTGCGCTTTCCAGTCGCGAAACCTGTGCTCCAGCTGCAT	3429
DB	183	TTAATTCGGTTGGCTCAGCTGCGCTTTCCAGTCGCGAAACCTGTGCTCCAGCTGCAT	242
QY	3430	TAATGAATCGGCCAAGCGCGGGAGAGCGGTTTGGTATTTGGGGCTCTTCGCTTCC	3489
DB	243	TAATGAATCGGCCAAGCGCGGGAGAGCGGTTTGGTATTTGGGGCTCTTCGCTTCC	302
QY	3490	TCGCTCACTAGCTGCTGCGCTCGTTCGCTGCGGTGCGGGAGCGGTATCAGCTCACTCA	3549
DB	303	TCGCTCACTAGCTGCTGCGCTCGTTCGCTGCGGTGCGGGAGCGGTATCAGCTCACTCA	362
QY	3550	AAGCGGTAAATAGCTTTATCCAGAGATCAGGGGATAACGACGAAAGACATGTGAGCA	3609
DB	363	AAGCGGTAAATAGCTTTATCCAGAGATCAGGGGATAACGACGAAAGACATGTGAGCA	422
QY	3610	AAAGGGCAGCAAAAGGCCAGGAACCGTAAAGAGCCGCTTGTGGCGTTTCCATAGG	3669
DB	423	AAAGGGCAGCAAAAGGCCAGGAACCGTAAAGAGCCGCTTGTGGCGTTTCCATAGG	482
QY	3670	CTCGGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCG	3729
DB	483	CTCGGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCG	542
QY	3730	ACAGGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCTTT	3789
DB	543	ACAGGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCTTT	602
QY	3790	CCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT	3849
DB	603	CCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT	662
QY	3850	TCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTTCGTTAGCTTCGCTCAAGCTGGC	3909
DB	663	TCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTTCGTTAGCTTCGCTCAAGCTGGC	722
QY	3910	TGTTGTGACGAAACCCCGCTTACCGGACCGCTGCGCTTATCCGGTAACTATGCTCTT	3969
DB	723	TGTTGTGACGAAACCCCGCTTACCGGACCGCTGCGCTTATCCGGTAACTATGCTCTT	782

QY	3970	GAGTCCAAACCCGGTAAAGACACGACTTATTCGCCACTGGCAGCAGCACTGGTAACAGATT	4029
DB	783	GAGTCCAAACCCGGTAAAGACACGACTTATTCGCCACTGGCAGCAGCACTGGTAACAGATT	842
QY	4030	AGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTTAACACGGC	4089
DB	843	AGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTTAACACGGC	902
QY	4090	TACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA	4149
DB	903	TACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA	962
QY	4150	AGAGTTGGTAGCTCTTGTATCCGGCAAAACAAACCAACCGCTGGTAGCGGTGTTTTGTT	4209
DB	963	AGAGTTGGTAGCTCTTGTATCCGGCAAAACAAACCAACCGCTGGTAGCGGTGTTTTGTT	1022
QY	4210	TGCAAGCAGCAGATTACGCGCAGAAAGAGATCTCAAGAGATCTTTGATCTTTCT	4269
DB	1023	TGCAAGCAGCAGATTACGCGCAGAAAGAGATCTCAAGAGATCTTTGATCTTTCT	1082
QY	4270	ACGGGGTCTGACGCTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATCGCGTCGAA	4329
DB	1083	ACGGGGTCTGACGCTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATCGCGTCGAA	1142
QY	4330	TCGGGAGCGCGATACCGTAAAGCAAGAGAGCGGTTCAGCCCATTCGCCCGCAAGCTCT	4389
DB	1143	TCGGGAGCGCGATACCGTAAAGCAAGAGAGCGGTTCAGCCCATTCGCCCGCAAGCTCT	1202
QY	4390	TCAGCAATATCAGCGGTAGCAACGCTATGTCTGTATAGCGGTCCGCCACACCCAGCGG	4449
DB	1203	TCAGCAATATCAGCGGTAGCAACGCTATGTCTGTATAGCGGTCCGCCACACCCAGCGG	1262
QY	4450	CCACAGTCATGAATCCAGAAAGCGCCATTTTCCACATGATATTCGGCAAGACAGGCA	4509
DB	1263	CCACAGTCATGAATCCAGAAAGCGCCATTTTCCACATGATATTCGGCAAGACAGGCA	1322
QY	4510	TCGCCATGGGTCAACGAGATCTTCGCCGTTCGGGATCGCGCTTCGAGCTTCGGCAAC	4569
DB	1323	TCGCCATGGGTCAACGAGATCTTCGCCGTTCGGGATCGCGCTTCGAGCTTCGGCAAC	1382
QY	4570	AGTTTCGGTGGCGGAGCGCTGATGCTCTTTCGTCCAGATCATCTGTATCGACAGCG	4629
DB	1383	AGTTTCGGTGGCGGAGCGCTGATGCTCTTTCGTCCAGATCATCTGTATCGACAGCG	1442
QY	4630	GCTTCATCCAGTACGTGCTCGTCGATGCGATGTTTCGTTGGTGGTGAATGGGCG	4689
DB	1443	GCTTCATCCAGTACGTGCTCGTCGATGCGATGTTTCGTTGGTGGTGAATGGGCG	1502
QY	4690	GTAGCCGATCAAGCGTATGACGCCCGCATTCGCATTCAGCCATGATGGATCTTTCTCG	4749
DB	1503	GTAGCCGATCAAGCGTATGACGCCCGCATTCGCATTCAGCCATGATGGATCTTTCTCG	1562
QY	4750	GCAGGAGAGGTGAGATGACAGGAGATCTTGCCTCCGCGCATTCGCGCCAAATAGAGCG	4809
DB	1563	GCAGGAGAGGTGAGATGACAGGAGATCTTGCCTCCGCGCATTCGCGCCAAATAGAGCG	1622
QY	4810	TCCTTCCCGCTTCAGTGACAGGTGACAGAGTCCGCAAGGAAACCGCCGCTGGGCC	4869
DB	1623	TCCTTCCCGCTTCAGTGACAGGTGACAGAGTCCGCAAGGAAACCGCCGCTGGGCC	1682
QY	4870	AGCCAGATAGCGCGCTGCTGCTTCAGTTCATTCAGGGCAACCGGACAGGTCCGTC	4929
DB	1683	AGCCAGATAGCGCGCTGCTGCTTCAGTTCATTCAGGGCAACCGGACAGGTCCGTC	1742
QY	4930	TTGACAAAAGAAACCGGGCGCCCTCGCTGACAGCCGGAACACCGCGGATCAGAGCAG	4989
DB	1743	TTGACAAAAGAAACCGGGCGCCCTCGCTGACAGCCGGAACACCGCGGATCAGAGCAG	1802
QY	4990	CCGATTTCTGTTGTCAGTCATAGCCGATAGCTCTCCACCCAAACCGCGCGGAGAA	5049
DB	1803	CCGATTTCTGTTGTCAGTCATAGCCGATAGCTCTCCACCCAAACCGCGCGGAGAA	1862
QY	5050	CCTGCGTCAATCCATCTTTGTTCAATCATGCGGAAACGATCTCTATCTCTCTTGATCA	5109

Db CCTGGTGCAATCATCTTGTTCATCATGGAACGATCCTCATCTGCTCTTGATCA 1922
Qy 5110 GATCTTGATCCCTGGCCATCAGATCCTTGGGGGGAAGAGCCATCCAGTTACTTTG 5169
Db 1923 GATCTTGATCCCTGGCCATCAGATCCTTGGGGGGAAGAGCCATCCAGTTACTTTG 1982
Qy 5170 CAGGGCTTCCCACTTACAGAGGGGCGCCAGCTGGCAATTCCGGTTCCGTTGCTGTGTC 5229
Db 1983 CAGGGCTTCCCACTTACAGAGGGGCGCCAGCTGGCAATTCCGGTTGCTGTGTC 2042
Qy 5230 CATAAAACCCGCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGGGGGCTCTTCGCTA 5289
Db 2043 CATAAAACCCGCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGGGGGCTCTTCGCTA 2102
Qy 5290 TTAGCCAGCTGGCGAAAGGGGGATGCTGTCAGAGGCGATTAAGTTGGGTAACGCCAGGG 5349
Db 2103 TTAGCCAGCTGGCGAAAGGGGGATGCTGTCAGAGGCGATTAAGTTGGGTAACGCCAGGG 2162
Qy 5350 TTTTCCAGTCACGACGTTGTAAACAGCGCCAGTCGAATTGTAATACGACTCACTATAG 5409
Db 2163 TTTTCCAGTCACGACGTTGTAAACAGCGCCAGTCGAATTGTAATACGACTCACTATAG 2222
Qy 5410 GCGCAATTGGAGCT 5423
Db 2223 GCGCAATTGGAGCT 2236

RESULT 6

AAV40796
ID AAV40796 standard; DNA; 3599 BP.
XX AC AAV40796;
XX DT 23-SEP-1998 (first entry)
XX DE Actual sequence of IGF-I containing plasmid pIG0552.
XX KW IGF-I; insulin-like growth factor I; skeletal alpha-actin gene promoter;
KW muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS;
KW Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
XX OS Synthetic.

XX XX

XX W09824922-A1.

XX 11-JUN-1998.

XX 01-DEC-1997; 97WO-US021852.

XX 02-DEC-1996; 96US-0031539P.

XX 19-NOV-1997; 97US-00974572.

XX (GENE-) GENEMEDICINE INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Coleman M, Schwartz R, Demayo FJ;

XX WPI; 1998-333339/29.

XX New vector for expression of insulin-like growth factor-I - containing a

XX skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3'

XX region from growth hormone 3'-UTR.

XX Claim 16; Page 37-41; 115pp; English.

XX This sequence is the actual sequence for pIG0552 which is an example of a

XX vector of the invention. The vector is for expression of a nucleic acid

XX sequence in a cell, and comprises: (a) a nucleic acid cassette containing

XX a sequence encoding insulin-like growth factor-I (IGF-I); (b) a 5'

XX flanking region including one or more sequences necessary for expression

XX of the nucleic acid cassette, including a promoter from a skeletal alpha-

XX actin gene; (c) a linker connecting the 5' flanking region to a nucleic

CC acid, the linker having a position for inserting the nucleic acid
CC cassette, and lacking the coding sequence of a gene with which it is
CC naturally associated; and (d) a 3' flanking region, including a 3'
CC untranslated region or a 3' non coding region or both, where the 3'
CC flanking region is 3' to the position for inserting the nucleic acid
CC cassette and comprises a sequence from a growth hormone 3'-UTR. The
CC vector can provide for efficient IGF-I expression, particularly in gene
CC therapy. It can be used for the delivery of IGF-I for treating diseases
CC such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth
CC disorders. They can be used for treating peripheral neuropathies
CC resulting from diabetes, genetic disease such as Type I or Type II
CC diabetes, genetic disease such as Chacot-marie-tooth disease, AIDS,
CC atherogenesis, atherosclerotic, cardiovascular, cerebrovascular, or
CC peripheral vascular disease, haemophilia, inflammation and side-effects
CC from anti-cancer and anti-viral drugs. The vectors can also be used to
CC create transgenic animals for research or livestock improvement
XX

SQ Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 U; 0 Other;

Query Match 40.9%; Score 2218; DB 2; Length 3599;

Best Local Similarity 99.6%; Pred. No. 3.7e-276;

Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTCAGCTTGGCG 3249
Db 3 GAGGGGGGGCGCGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTCAGCTTGGCG 62
Qy 3250 TAATCATGTCATAGCTGTTTCTGCTGTGAAATGTTATCCGCTCACAANTTCCACAAC 3309
Db 63 TAATCATGTCATAGCTGTTTCTGCTGTGAAATGTTATCCGCTCACAANTTCCACAAC 122
Qy 3310 ATACGAGCGGAAGCATAAAGTGTAAAGCTGGGGTGCCCTAAATGAGTGAGCTAACTCACA 3369
Db 123 ATACGAGCGGAAGCATAAAGTGTAAAGCTGGGGTGCCCTAAATGAGTGAGCTAACTCACA 182
Qy 3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTTCGGGAAAACCTGTGCGCGAGCTGCAT 3429
Db 183 TTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTTCGGGAAAACCTGTGCGCGAGCTGCAT 242
Qy 3430 TAATGAATCGGCCAAGCGCGGGGAGGGGTTGGTATGGGGCTCTTCGCGTTCC 3489
Db 243 TAATGAATCGGCCAAGCGCGGGGAGGGGTTGGTATGGGGCTCTTCGCGTTCC 302
Qy 3490 TCGCTCACTCACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCACTCA 3549
Db 303 TCGCTCACTCACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCACTCA 362
Qy 3550 AAGCGGTAATAGCGTTATCCAGAAATCAGGGGATAACCGAGGAAGAAACATGTAGCA 3609
Db 363 AAGCGGTAATAGCGTTATCCAGAAATCAGGGGATAACCGAGGAAGAAACATGTAGCA 422
Qy 3610 AAGGCCAGCAAAAGGCCAGGNAACCGTAAAGGCGCGCTTGTGGGTTTTTCCATAGG 3669
Db 423 AAGGCCAGCAAAAGGCCAGGNAACCGTAAAGGCGCGCTTGTGGGTTTTTCCATAGG 482
Qy 3670 CTCGCCCCCTCGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCG 3729
Db 483 CTCGCCCCCTCGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCG 542
Qy 3730 ACAGGACTATAAAGATACCAAGGCGTTTCCCGCTGGAAAGCTCCCTCGTGGCTCTCTGTT 3789
Db 543 ACAGGACTATAAAGATACCAAGGCGTTTCCCGCTGGAAAGCTCCCTCGTGGCTCTCTGTT 602
Qy 3790 CCGACCTTGGCGCTTACGGGATACCTGTCGCGCTTCTCCCTTGGGAAGGCGTGGCGCTT 3849
Db 603 CCGACCTTGGCGCTTACGGGATACCTGTCGCGCTTCTCCCTTGGGAAGGCGTGGCGCTT 662
Qy 3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTCTGTTCCGCTCCAAGCTGGGC 3909
Db 663 TCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTCTGTTCCGCTCCAAGCTGGGC 722
Qy 3910 TGTGTGACGAAACCCCGCTTACGCCGACGCGCTGCGGCTTATCCGGTAACTATGCTTT 3969
Db

Db	723	TGTTGTGACGAACCCCGCTTCACGCCGACCGCTGCGCGCTTATCCGGTAACTATCGTCTT	782
Qy	3970	GAGTCCAAACCCGGTAAGACACGACTTATCGCACTGGCAGCAGCACTGGTAAACAGGATT	4029
Db	783	GAGTCCAAACCCGGTAAGACACGACTTATCGCACTGGCAGCAGCACTGGTAAACAGGATT	842
Qy	4030	AGCAGAGCGAGGTATGTAGGCGGTGCTTACAGAGTTCCTTGAAGTGGTGGCTTAACACGGC	4089
Db	843	AGCAGAGCGAGGTATGTAGGCGGTGCTTACAGAGTTCCTTGAAGTGGTGGCTTAACACGGC	902
Qy	4090	TACACTAGAGAAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGATTACTTCGGAAAA	4149
Db	903	TACACTAGAGAAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGATTACTTCGGAAAA	962
Qy	4150	AGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGCTAGCGGTGGTTTTTGTGTT	4209
Db	963	AGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGCTAGCGGTGGTTTTTGTGTT	1022
Qy	4210	TGCAAGCAGCAGATTACCGCGCAGAAAAAAAGGATCTCAAGAAGATCTTTTGATCTTTTCT	4269
Db	1023	TGCAAGCAGCAGATTACCGCGCAGAAAAAAAGGATCTCAAGAAGATCTTTTGATCTTTTCT	1082
Qy	4270	ACGGGCTCTGACGCTCAGAGAACTCTCAAGAGGCGATAGAGGCGATGCGCTGCGAA	4329
Db	1083	ACGGGCTCTGACGCTCAGAGAACTCTCAAGAGGCGATAGAGGCGATGCGCTGCGAA	1142
Qy	4330	TCGGGAGCGGCGATACCGTTAAAGCAGAGGAAGCGGTCAAGCCATTCGCCGCCAAGCTCT	4389
Db	1143	TCGGGAGCGGCGATACCGTTAAAGCAGAGGAAGCGGTCAAGCCATTCGCCGCCAAGCTCT	1202
Qy	4390	TCAGCAATATCACGGGTAGCCAAACGCTATGTCTTGATAGCGGTCCGCCAACCCAGCCGG	4449
Db	1203	TCAGCAATATCACGGGTAGCCAAACGCTATGTCTTGATAGCGGTCCGCCAACCCAGCCGG	1262
Qy	4450	CCACAGTCGATGAATCCAGAAAAAGCGCCATTTTCCACCAATGATATTCGGCAGCAGGCA	4509
Db	1263	CCACAGTCGATGAATCCAGAAAAAGCGCCATTTTCCACCAATGATATTCGGCAGCAGGCA	1322
Qy	4510	TCGGCATGGGTCAAGCAGATCCTCGCGTCGGGCATGCGCGCTTGAGCCTTGGCGAAC	4569
Db	1323	TCGGCATGGGTCAAGCAGATCCTCGCGTCGGGCATGCGCGCTTGAGCCTTGGCGAAC	1382
Qy	4570	AGTTGCGCTGGCGGAGCCCTGATGCTTCTGTFCCAGATCATCTGATCGACAAGACCG	4629
Db	1383	AGTTGCGCTGGCGGAGCCCTGATGCTTCTGTFCCAGATCATCTGATCGACAAGACCG	1442
Qy	4630	GCTTCCATCCGAGTACGTGCTCGATCGGATGTTTTCGTTGGTGGTTCGAATGGCGAG	4689
Db	1443	GCTTCCATCCGAGTACGTGCTCGATCGGATGTTTTCGTTGGTGGTTCGAATGGCGAG	1502
Qy	4690	GTAGCCGATCAAGCGTATGACGCGCGCATTTGATTCAGCCATGATGATCTTTCTCG	4749
Db	1503	GTAGCCGATCAAGCGTATGACGCGCGCATTTGATTCAGCCATGATGATCTTTCTCG	1562
Qy	4750	GCAGGACAAAGTGAGATGACAGGAGATCCTGCGCCCGGCATTCGCCCAAATAGCAGCCAG	4809
Db	1563	GCAGGACAAAGTGAGATGACAGGAGATCCTGCGCCCGGCATTCGCCCAAATAGCAGCCAG	1622
Qy	4810	TCCCTTCCGGTTCAGTGAACAGTGCAGACACAGCTCGGCAAGGAACGCCCGCTGTGGCC	4869
Db	1623	TCCCTTCCGGTTCAGTGAACAGTGCAGACACAGCTCGGCAAGGAACGCCCGCTGTGGCC	1682
Qy	4870	AGCCACGATAGCCGCGTCTGCTGCTGAGATTCATTTCAAGGCGACCGGACAGCTGGTC	4929
Db	1683	AGCCACGATAGCCGCGTCTGCTGCTGAGATTCATTTCAAGGCGACCGGACAGCTGGTC	1742
Qy	4930	TTGACAAAAGAACCGGCGCCCTCGCTGAGCAGCCGGAACCGCGGCGATCAGAGCAG	4989
Db	1743	TTGACAAAAGAACCGGCGCCCTCGCTGAGCAGCCGGAACCGCGGCGATCAGAGCAG	1802
Qy	4990	CCGATTGTCTTGTGCGCAGTCAATAGCCGAATAGCTCTTCCACCCAAAGCGCGCGAGAA	5049
Db	1803	CCGATTGTCTTGTGCGCAGTCAATAGCCGAATAGCTCTTCCACCCAAAGCGCGCGAGAA	1862

Qy	5050	CCTGCGTGCAAATCAATCTTTGTTCAAATCATGCGAAAACGATCCTCATCTGTCTCTTGATCA	5109
Db	1863	CCTGCGTGCAAATCCATCTTTGTTCAAATCATGCGAAAACGATCCTCATCTGTCTCTTGATCA	1922
Qy	5110	GATCTTCAGTCCCCTGGGCCAATCAGATCCTTTGGCGGCAAGAAGCCATCCAGTTTACTTTTG	5169
Db	1923	GAICTTTGATCCCCTGGGCCAATCAGATCCTTTGGCGGCAAGAAGCCATCCAGTTTACTTTTG	1982
Qy	5170	CAGGGCTTCCCAACCTTTAACAGAGGGCGCCCCAGCTGGGCAATTCCGGTTTCGCTTGTCTGTC	5229
Db	1983	CAGGGCTTCCCAACCTTTTACCAGAGGGCGCCCCAGCTGGGCAATTCCGGTTTCGCTTGTCTGTC	2042
Qy	5230	CATAAAACCCGCCAGCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGGCTCTTCGCTA	5289
Db	2043	CATAAAACCCGCCAGCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGGCTCTTCGCTA	2102
Qy	5290	TTACGCCAGCTGGCGAAAGGGCGATGTCTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGG	5349
Db	2103	TTACGCCAGCTGGCGAAAGGGGGAATGTCTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGG	2162
Qy	5350	TTTTTCCAGTCACGAGCTTGTATAAACAAGCGCCAGTGAAATTGTAATACGACTCACTATAG	5409
Db	2163	TTTTTCCAGTCACGAGCTTGTATAAACAAGCGCCAGTGAAATTGTAATACGACTCACTATAG	2222
Qy	5410	GGCGAATTGGAGCT 5423	
Db	2223	GGCGAATTGGAGCT 2236	
RESULT 7			
ADS73974			
ID	ADS73974 standard; DNA; 3803 BP.		
XX	ADS73974;		
XX	16-DEC-2004 (first entry)		
DT			
DE	Plasmid pAV2002 nucleotide sequence.		
XX			
KW	IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEP-2; TGF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis; vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic; cardiant; vasotropic; ophthalmological; cerebroprotective; ds.		
KW			
KW			
XX	Synthetic.		
OS			
XX	WO2004081040-A2.		
PN			
XX	23-SEP-2004.		
PD			
XX			
PF	11-MAR-2004; 2004WO-US007295.		
XX			
PR	12-MAR-2003; 2003US-0454079P.		
XX			
PA	(ADVI-) ADVISYS INC.		
PA	(BAYU) BAYLOR COLLEGE MEDICINE.		
XX			
Pi	Rabinovsky ED, Draghia-Akli R;		
XX			
DR	WPI; 2004-668935/65.		
XX			
PT	New isolated nucleic acid expression construct having a myogenic promoter, a nucleic acid sequence encoding IGF-IIe, and a 3'UTR, useful for treating diabetes, ischemic heart and cerebrovascular disease.		
FT			
PT			
XX	Claim 11; SEQ ID NO 2; 104pp; English.		
PS			
XX			
CC	The invention relates to an isolated nucleic acid expression construct comprising a myogenic promoter, a nucleic acid sequence encoding an insulin-like growth factor I (IGF-I) or its functional biological equivalent, and a 3' untranslated region (3'UTR), which has in vivo expression activity for the encoded IGF-I in a tissue. The myogenic		
CC			


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Db 919 GTATTGTTGTAATCTGCGCTCTGCTGAGCCAGTACCTTCGGAAGAGAGTGTGAGCTCT 978
QY 4165 TGATCGGCGAAACAAACACCGCTGTGTAGCGGTGTTTTTTTGTGTCGAAGCAGAGATT 4224
Db 979 TGATCGGCGAAACAAACACCGCTGTGTAGCGGTGTTTTTTTGTGTCGAAGCAGAGATT 1038
QY 4225 ACGGCGAGAAAAGAGATCTCAAGAGATCCCTTTGATCTTTTCTACGGGGTCTGACGCT 4284
Db 1039 ACGGCGAGAAAAGAGATCTCAAGAGAGATCCCTTTGATCTTTTCTACGGGGTCTGACGCT 1098
QY 4285 CAGAGAATCTCGTCAAGAGCGCATAGAGCGCATGCGCTGCGCAATCGGAGCGGGCGATA 4344
Db 1099 CAGAGAACTCGTCAAGAGCGCATAGAGCGCATGCGCTGCGCAATCGGAGCGGGCGATA 1158
QY 4345 CCCTAAAGCAGAGAGCGGTGAGCCCATTCGCCGCCAAGCTCTTCAGCAATATACAGG 4404
Db 1159 CCCTAAAGCAGAGAGCGGTGAGCCCATTCGCCGCCAAGCTCTTCAGCAATATACAGG 1218
QY 4405 GTAGCCAAACGTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCCACAGTCGATGAAT 4464
Db 1219 GTAGCCAAACGTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCCACAGTCGATGAAT 1278
QY 4465 CCAGAAAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAAG 4524
Db 1279 CCAGAAAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAAG 1338
QY 4525 ACAGATCTCTCGCGTCGGGATGCGCGCTTGAGCTGCGCAACAGTTCGGCTGGCGCG 4584
Db 1339 ACAGATCTCTCGCGTCGGGATGCGCGCTTGAGCTGCGCAACAGTTCGGCTGGCGCG 1398
QY 4585 AGCCCTGATGCTCTTCGTCCAGTATCTCTGATGCGCAAGCAGCGGCTTCATCCGAGTA 4644
Db 1399 AGCCCTGATGCTCTTCGTCCAGTATCTCTGATGCGCAAGCAGCGGCTTCATCCGAGTA 1458
QY 4645 CGTCTCGCTCGATGCGCATGTTTCGCTTGGTGGTTCGAATGGGCGAGGTAGCGGATCAAGC 4704
Db 1459 CGTCTCGCTCGATGCGCATGTTTCGCTTGGTGGTTCGAATGGGCGAGGTAGCGGATCAAGC 1518
QY 4705 GTATGACGCGCGCATTCGATCAGCCATGATGATATCTTCTCGGCGAGGAGCAAGTGA 4764
Db 1519 GTATGACGCGCGCATTCGATCAGCCATGATGATATCTTCTCGGCGAGGAGCAAGTGA 1578
QY 4765 GATGACAGGAGATCTCTCGCGCGCACTTCGCCCAATAGCAGCGATCCCTTCCGCTTCA 4824
Db 1579 GATGACAGGAGATCTCTCGCGCGCACTTCGCCCAATAGCAGCGATCCCTTCCGCTTCA 1638
QY 4825 GTGACAACTGTCAGCAGCTGCGCAAGGAAACGCGCTCGTGGCGCAGCCAGTAGCCGC 4884
Db 1639 GTGACAACTGTCAGCAGCTGCGCAAGGAAACGCGCTCGTGGCGCAGCCAGTAGCCGC 1698
QY 4885 GCTGCTCTGCTCTGAGTTCATTCAGGGCACCGGACAGGTGCTTTGACAAAAGAAC 4944
Db 1699 GCTGCTCTGCTCTGAGTTCATTCAGGGCACCGGACAGGTGCTTTGACAAAAGAAC 1758
QY 4945 GGGCGCCCTCGCTGACAGCGGAAACACGCGCGCATCAGACGCGATGCTGTTGT 5004
Db 1759 GGGCGCCCTCGCTGACAGCGGAAACACGCGCGCATCAGACGCGATGCTGTTGT 1818
QY 5005 GCCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTCAATCCA 5064
Db 1819 GCCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTCAATCCA 1878
QY 5065 TCTTGTTCATATCATCGAAACGATCTCATCTCTCTCTTGTATCAGATCTTTGATCCCTG 5124
Db 1879 TCTTGTTCATATCATCGAAACGATCTCATCTCTCTCTTGTATCAGATCTTTGATCCCTG 1938
QY 5125 CGCATCATGATCTCTTGGCGGAAAGACCATTCAGTTTACTTTGAGGGCTTCCCAACC 5184
Db 1939 CGCATCATGATCTCTTGGCGGAAAGACCATTCAGTTTACTTTGAGGGCTTCCCAACC 1998
QY 5185 TTACACAGGGCGCCAGCTGGCAATTCGGGTTGCTGTCCTTCCATATAAACCGCCAG 5244
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Db 1999 TTACCAGAGGGGCCCCAGCTGGCAATTCGGTTCGCTTGTCCATAAAACGCCCCAG 2058
QY 5245 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTTACGCCAGCTGGCG 5304
Db 2059 TCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTTACGCCAGCTGGCG 2118
QY 5305 AAAGGGGGATGCTCTGCAAGGGCGATTAAAGTTGGGTAAACGCCAGGGTTTCCCAAGTCA 5364
Db 2119 AAAGGGGGATGCTCTGCAAGGGCGATTAAAGTTGGGTAAACGCCAGGGTTTCCCAAGTCA 2178
QY 5365 CGTTGTAACACGACGCCAGTGAATTTGTAATACGATCTACTATAGGCGGAATTTGGAGCT 5423
Db 2179 CGTTGTAACACGACGCCAGTGAATTTGTAATACGATCTACTATAGGCGGAATTTGGAGCT 2237

RESULT 9
AAV40795
ID AAV40795 standard; DNA; 3600 BP.
XX
AC AAV40795;
XX
XX 23-SBP-1998 (first entry)
XX
DE Expected sequence of IGF-I containing plasmid pIG0552.
XX
XX IGF-I; insulin-like growth factor I; skeletal alpha-actin gene promoter;
XX muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS;
XX Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
XX Synthetic.
XX
XX WO9824922-A1.
XX
XX 11-JUN-1998.
XX
XX 01-DEC-1997; 97WO-US021852.
XX
XX 02-DEC-1996; 96US-0031539P.
XX 19-NOV-1997; 97US-00974572.
XX
XX (GENE-) GENEMEDICINE INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Coleman M, Schwartz R, Demayo FJ;
XX
XX WPI; 1998-333339/29.
XX
XX New vector for expression of insulin-like growth factor-I - containing a
XX skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3'
XX region from growth hormone 3'-UTR.
XX
XX Claim 16; Page 37-41; 115pp; English.
XX
XX This sequence is the expected sequence for pIG0552 which is an example of
XX a vector of the invention. The vector is for expression of a nucleic acid
XX sequence in a cell, and comprises: (a) a nucleic acid cassette containing
XX a sequence encoding insulin-like growth factor-I (IGF-I); (b) a 5'
XX flanking region including one or more sequences necessary for expression
XX of the nucleic acid cassette, including a promoter from a skeletal alpha-
XX actin gene; (c) a linker connecting the 5' flanking region to a nucleic
XX acid, the linker having a position for inserting the nucleic acid
XX cassette, and lacking the coding sequence of a gene with which it is
XX naturally associated; and (d) a 3' flanking region, including a 3'
XX untranslated region or a 3' non coding region or both, where the 3'
XX flanking region is 3' to the position for inserting the nucleic acid
XX cassette and comprises a sequence from a growth hormone 3'-UTR. The
XX vector can provide for efficient IGF-I expression, particularly in gene
XX therapy. It can be used for the delivery of IGF-I for treating diseases
XX such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth
XX disorders. They can be used for treating peripheral neuropathies
XX resulting from diabetes, genetic disease such as Type I or Type II
XX diabetes, genetic disease such as Chacot-marie-tooth disease, AIDS,
XX atherogenesis, atherosclerotic, cardiovascular, cerebrovascular, or
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CC peripheral vascular disease, haemophilia, inflammation and side-effects
CC from anti-cancer and anti-viral drugs. The vectors can also be used to
CC create transgenic animals for research or livestock improvement
XX
SQ Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 U; 0 Other;
Query Match 40.9%; Score 2215.8; DB 2; Length 3600;
Best Local Similarity 99.9%; Pred. No. 7e-276;
Matches 2217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3205 CTGAGCTTTTGTCCCTTTAGTGGGGTTAAATTCGAGCTTGGGTAATCATGCTCATAG 3264
DB 19 CCAGAGCTTTTGTCCCTTTAGTGGGGTTAAATTCGAGCTTGGGTAATCATGCTCATAG 78
QY 3265 CTGTTTCTCTGTGAAATTGTATCCGCTCAACAATTCACACAACATACGAGCGGAAGC 3324
DB 79 CTGTTTCTCTGTGAAATTGTATCCGCTCAACAATTCACACAACATACGAGCGGAGC 138
QY 3325 ATAAAGTGAAGCTGGGTGCTTAATGAGTGAGCTAACTCAATTAATTTGGTTGGCG 3384
DB 139 ATAAAGTGAAGCTGGGTGCTTAATGAGTGAGCTAACTCAATTAATTTGGTTGGCG 198
QY 3385 TCACTGCCCGCTTTCAGTCGGGAAACCTGCTGCGCAGCTGCATTAATGAATCGGCCAA 3444
DB 199 TCACTGCCCGCTTTCAGTCGGGAAACCTGCTGCGCAGCTGCATTAATGAATCGGCCAA 258
QY 3445 CGCGCGGGAGAGCGGTTTTCGCTATTGGGCGCTCTTCGCTTCCCTGCTCACTGACTCG 3504
DB 259 CGCGCGGGAGAGCGGTTTTCGCTATTGGGCGCTCTTCGCTTCCCTGCTCACTGACTCG 318
QY 3505 CTGCGCTCGGTTCGCGCTGCGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 3564
DB 319 CTGCGCTCGGTTCGCGCTGCGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG 378
QY 3565 TTATCCACAGAAATCAGGGGATAACGAGGAAAGAAATGAGGAGAAAGGCCAGGAAAG 3624
DB 379 TTATCCACAGAAATCAGGGGATAACGAGGAAAGAAATGAGGAGAAAGGCCAGGAAAG 438
QY 3625 GCCAGGAACCGTAAAGGCGCGTTCGCTGCGCTTTTTCATAGGCTCGCCCCCTTGAC 3684
DB 439 GCCAGGAACCGTAAAGGCGCGTTCGCTGCGCTTTTTCATAGGCTCGCCCCCTTGAC 498
QY 3685 GAGCATCAAAAAATCAGCGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAGA 3744
DB 499 GAGCATCAAAAAATCAGCGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAGA 558
QY 3745 TACAGCGGTTTCCCTCTGGAAGCTCCCTCGTGGGTCTCTCTGTTCGACCCCTGCGCTT 3804
DB 559 TACAGCGGTTTCCCTCTGGAAGCTCCCTCGTGGGTCTCTCTGTTCGACCCCTGCGCTT 618
QY 3805 ACCGGATACCTGTCCGCTTTCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGC 3864
DB 619 ACCGGATACCTGTCCGCTTTCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGC 678
QY 3865 TGTAGGTATCTCAGTTCCGTTGAGGTGTTCCGCTCCAAAGCTGGGCTGTGTGACGAAACC 3924
DB 679 TGTAGGTATCTCAGTTCCGTTGAGGTGTTCCGCTCCAAAGCTGGGCTGTGTGACGAAACC 738
QY 3925 CCCGTTACGCCGACCGCTCGGCTTATCCGGTAACTATCGTTTGAATCCAAACCGGTA 3984
DB 739 CCCGTTACGCCGACCGCTCGGCTTATCCGGTAACTATCGTTTGAATCCAAACCGGTA 798
QY 3985 AGACAGACTTATCGCCACTGGGAGCGCCACTGGTAAACAGGATTAGCAGAGCGAGGTAT 4044
DB 799 AGACAGACTTATCGCCACTGGGAGCGCCACTGGTAAACAGGATTAGCAGAGCGAGGTAT 858
QY 4045 GTAGGCGGTCTACAGAGTTCTTGAAGTGGTGGCTAACTACCGGCTACACTAGAAGAACA 4104
DB 859 GTAGGCGGTCTACAGAGTTCTTGAAGTGGTGGCTAACTACCGGCTACACTAGAAGAACA 918
QY 4105 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 4164
DB 919 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT 978

QY 4165 TGATCGGCAAAACAAACACCGCTGCTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATT 4224
DB 979 TGATCGGCAAAACAAACACCGCTGCTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATT 1038
QY 4225 ACAGCGAGAAAAAAGAGTCTCAAGAGATCTTTTGTATCTTTTCTACGGGCTTCAGCCT 4284
DB 1039 ACAGCGAGAAAAAAGAGTCTCAAGAGATCTTTTGTATCTTTTCTACGGGCTTCAGCCT 1098
QY 4285 CAGAAGAACTCGTCAAGAAAGCGGATAGAGGCGATCGCTGCGAATCGGAGCGGCGGATA 4344
DB 1099 CAGAAGAACTCGTCAAGAAAGCGGATAGAGGCGATCGCTGCGAATCGGAGCGGCGGATA 1158
QY 4345 CCCTAAAGCACAGAGGAAGCGGTGAGCCCATTTCCGCGCCAGCTCTTCAGCAATATCACGG 4404
DB 1159 CCCTAAAGCACAGAGGAAGCGGTGAGCCCATTTCCGCGCCAGCTCTTCAGCAATATCACGG 1218
QY 4405 GTAGCAAAAGCTATGTCCTGATAGCGGTTCGCCACACCCAGCGGCCACAGTGCATGAAT 4464
DB 1219 GTAGCAAAAGCTATGTCCTGATAGCGGTTCGCCACACCCAGCGGCCACAGTGCATGAAT 1278
QY 4465 CCAGAAAGCGGCGCATTTTCCACCATGATATTCGCGCAAGCAGGATCGCCATGGGTCAAG 4524
DB 1279 CCAGAAAGCGGCGCATTTTCCACCATGATATTCGCGCAAGCAGGATCGCCATGGGTCAAG 1338
QY 4525 ACAGATCTCTCGCGTGGGCGATGCGCGCTTGAGCTTGGCGAACAGTTCCGGCTGGCGCG 4584
DB 1339 ACAGATCTCTCGCGTGGGCGATGCGCGCTTGAGCTTGGCGAACAGTTCCGGCTGGCGCG 1398
QY 4585 AGCCCTGATGCTTTTCTGTCAGATCATCTGATCGAACAAGCCGGCTTCATCCGAGTA 4644
DB 1399 AGCCCTGATGCTTTTCTGTCAGATCATCTGATCGAACAAGCCGGCTTCATCCGAGTA 1458
QY 4645 CGTGTCTGCTCGATGCGATGTTTTCGCTTGGTGTGAAATGGGCGAGTTCAGCGGATCAAG 4704
DB 1459 CGTGTCTGCTCGATGCGATGTTTTCGCTTGGTGTGAAATGGGCGAGTTCAGCGGATCAAG 1518
QY 4705 GTATGAGCGCGCGCATGTCATCAGCCATGATGGATCTTCTCGGAGGAGCAAGGTGA 4764
DB 1519 GTATGAGCGCGCGCATGTCATCAGCCATGATGGATCTTCTCGGAGGAGCAAGGTGA 1578
QY 4765 GATGACAGGAGATCTTCCCGCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCA 4824
DB 1579 GATGACAGGAGATCTTCCCGCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCA 1638
QY 4825 GTGACAAAGTTCGAGCAAGTTCGCGCAAGGAAACCGCGTTCGTGCGCAGCCAGTAGCCGC 4884
DB 1639 GTGACAAAGTTCGAGCAAGTTCGCGCAAGGAAACCGCGTTCGTGCGCAGCCAGTAGCCGC 1698
QY 4885 GCTGCTCTGCTCGCTGATTCATTCAGGGCAACCGGACAGGTCGGTCTTGACAAAAAGAAC 4944
DB 1699 GCTGCTCTGCTCGCTGATTCATTCAGGGCAACCGGACAGGTCGGTCTTGACAAAAAGAAC 1758
QY 4945 GGGCGCCCTCGCTGACAGCCGGAACACGGGGCATCAAGCAGCGGATTTGTCTGTGTGT 5004
DB 1759 GGGCGCCCTCGCTGACAGCCGGAACACGGGGCATCAAGCAGCGGATTTGTCTGTGTGT 1818
QY 5005 GCCAGTTCATAGCGGAATAGCTCTCCACCAAGCGCGCGGAGAACTGCGTGCATCCA 5064
DB 1819 GCCAGTTCATAGCGGAATAGCTCTCCACCAAGCGCGCGGAGAACTGCGTGCATCCA 1878
QY 5065 TCTTGTTCATCATGCGAAACGATCTCATCTCTCTTGTCTTGTATCAGATCTTGTATCCCTG 5124
DB 1879 TCTTGTTCATCATGCGAAACGATCTCATCTCTCTTGTCTTGTATCAGATCTTGTATCCCTG 1938
QY 5125 CGCCATCAGATCTTGGCGGCAAGAGCCATCCAGTTTACTTTTGCAGGGCTTTCCCAACC 5184
DB 1939 CGCCATCAGATCTTGGCGGCAAGAGCCATCCAGTTTACTTTTGCAGGGCTTTCCCAACC 1998
QY 5185 TTACAGAGGGCGCCCGCAGTGGCAATTCGGGTTTCGGTTGCTGTCTCATATAAAACCGGCCAG 5244
DB 1999 TTACAGAGGGCGCCCGCAGTGGCAATTCGGGTTTCGGTTGCTGTCTGTCTCATATAAAACCGGCCAG 2058

QY 5245 TCTAGCAACTGTGTGGGAAGGCGATCGGTGCGGCGCTCTTCGCTATTACGCCAGCTGGCG 5304
DB 2059 TCTAGCAACTGTGTGGGAAGGCGATCGGTGCGGCGCTCTTCGCTATTACGCCAGCTGGCG 2118
QY 5305 AAAGGGGGATGTGCTGCAAGCGCATTAAGTTGGGTAAAGCCAGGTTTCCCAAGTACGA 5364
DB 2119 AAAGGGGGATGTGCTGCAAGCGCATTAAGTTGGGTAAAGCCAGGTTTCCCAAGTACGA 2178
QY 5365 CGTTGTAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 5423
DB 2179 CGTTGTAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCT 2237

RESULT 10
AAL60457
ID AAL60457 standard; DNA; 3558 BP.
AC AAL60457;
XX 27-AUG-2003 (first entry)
XX pGR1774 plasmid comprising human (1-40) GHRH DNA.
DE Growth hormone releasing hormone; GHRH; lean body mass; bone density;
KW bone healing; gene therapy; anorectic; osteopathic; circular; cyclic;
KW human; ds.
XX Homo sapiens.
XX WO2003038112-A2.
XX 08-MAY-2003.
XX 25-OCT-2002; 2002WO-US034275.
XX 26-OCT-2001; 2001US-0357808P.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX Draghia-Akli R, Schwartz RJ;
FI WPI; 2003-493212/46.
XX Decreasing body fat proportion, increasing lean body mass, bone density
PT or bone healing rate by delivering into cells of the subject a nucleic
PT acid expression construct that encodes a growth-hormone-releasing-hormone
PT (GHRH).
XX Claim 30; Page 160-162; 165pp; English.
XX The invention relates to a method for decreasing body fat proportion,
CC increasing lean body mass, bone density or bone healing rate in a subject
CC which involves delivering a nucleic acid expression construct that
CC encodes a growth hormone releasing hormone (GHRH) or its functional
CC biological equivalent into cells of the subject. The method is useful for
CC decreasing body fat proportion, for increasing lean body mass, bone
CC density or bone healing rate, or for altering lean body mass in a
CC subject. It is used in gene therapy. The present sequence is a pGR1774
CC plasmid comprising human (1-40) GHRH DNA. This sequence is used to
CC illustrate the method of the invention
XX
SQ Sequence 3558 BP; 774 A; 1018 C; 949 G; 816 T; 0 U; 1 Other;

Query Match 40.8%; Score 2211.6; DB 9; Length 3558;
Best Local Similarity 99.5%; Pred. No. 2.4e-275;
Matches 2217; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3190 GAGCCAGGACAGCTCAGCTTTGTTCCCTTTAGTGAGGGTTAAATTGAGCTTGGCG 3249
DB 1200 GAGGGGGGCGCGGTACAGCTTTTGTTCCTTTAGTGAGGGTTAAATTGAGCTTGGCG 1259
QY 3250 TAATCATGGTCATAGCTGTTTCCCTGTGTGAAATTGTTATCCGCTCACAAATTCACACAAC 3309

DB 1260 TAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAAATTCACACAAC 1319
QY 3310 ATACGAGCCGGAAGCATATAAGTGTAAAGCCTGGGGTGCCTTAATGAGTAGCTAACTCACCA 3369
DB 1320 ATACGAGCCGGAAGCATATAAGTGTAAAGCCTGGGGTGCCTTAATGAGTAGCTAACTCACCA 1379
QY 3370 TTAATTGCGTTGCGCTCACCTGCCCCCTTTTCAGTCGGGAAAACCTGTGTCGCGAGCTGCAT 3429
DB 1380 TTAATTGCGTTGCGCTCACCTGCCCCCTTTTCAGTCGGGAAAACCTGTGTCGCGAGCTGCAT 1439
QY 3430 TAATGAATCGGCCAAACGCGCGGGAGAGCGGTTTGGTATTGGGGCGCTCTTCGCGCTTCC 3489
DB 1440 TAATGAATCGGCCCAACGCGCGGGAGAGCGGTTTGGTATTGGGGCGCTCTTCGCGCTTCC 1499
QY 3490 TCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGCGAGCGGTATCAGCTCACTCA 3549
DB 1500 TCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGCGAGCGGTATCAGCTCACTCA 1559
QY 3550 AAGCGGTATATACGGTTATCCACAGAAATCAGGGGATAACACGAGAAAGACATGTGAGCA 3609
DB 1560 AAGCGGTATATACGGTTATCCACAGAAATCAGGGGATAACACGAGAAAGACATGTGAGCA 1619
QY 3610 AAAGCCAGCAAAAAGCCAGGAACCGTAAAAAGCCGCTTCTGGCGTTTTCATAGG 3669
DB 1620 AAAGCCAGCAAAAAGCCAGGAACCGTAAAAAGCCGCTTCTGGCGTTTTCATAGG 1679
QY 3670 CTCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
DB 1680 CTCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1739
QY 3730 ACAGGACTATAAAGATACCAAGCGTTTCCCTTGGAAAGTCCCTCGTGGCGCTCTCTGTT 3789
DB 1740 ACAGGACTATAAAGATACCAAGCGTTTCCCTTGGAAAGTCCCTCGTGGCGCTCTCTGTT 1799
QY 3790 CCGACCTCGCGCTTACCGGATACCTGTCGCGCTTCTCCCTCGGGAAGCGTGGCGTT 3849
DB 1800 CCGACCTCGCGCTTACCGGATACCTGTCGCGCTTCTCCCTCGGGAAGCGTGGCGTT 1859
QY 3850 TCTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTCTGTTCCCTCAAGCTGGGC 3909
DB 1860 TCTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTCTGTTCCCTCAAGCTGGGC 1919
QY 3910 TGTGTGCAAGAACCCCGCTTACGCGACCGCTGCGCTTATCCGGTAACTATCGTCTT 3969
DB 1920 TGTGTGCAAGAACCCCGCTTACGCGACCGCTGCGCTTATCCGGTAACTATCGTCTT 1979
QY 3970 GAGTCCAAACCCGGTAAAGACAGCTATTCGCACTGCGCAGCAGCCACTGGTAAAGGATT 4029
DB 1980 GAGTCCAAACCCGGTAAAGACAGCTATTCGCACTGCGCAGCAGCCACTGGTAAAGGATT 2039
QY 4030 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGCGCTTAACCTACGGC 4089
DB 2040 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGCGCTTAACCTACGGC 2099
QY 4090 TACACTAGAGAAACAGTATTGTTGTTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAATA 4149
DB 2100 TACACTAGAGAAACAGTATTGTTGTTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAATA 2159
QY 4150 AGAGTTGGTGTGTTGATCCGCGCAAAACAAACCAACCGCTGTAGCGGTGTTTTTTGTT 4209
DB 2160 AGAGTTGGTGTGTTGATCCGCGCAAAACAAACCAACCGCTGTAGCGGTGTTTTTTGTT 2219
QY 4210 TGCAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGTCTTTGATCTTTTCT 4269
DB 2220 TGCAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGTCTTTGATCTTTTCT 2279
QY 4270 ACCGGGTCTGACGCTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAAGCGGATCGCTCGGAA 4329
DB 2280 ACCGGGTCTGACGCTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAAGCGGATCGCTCGGAA 2339
QY 4330 TCGGAGCGGCGATACCGTTAAAGCAACGAGGAGCGGTGAGCCCATTTGCGCCCAAGCTCT 4389
DB 2340 TCGGAGCGGCGATACCGTTAAAGCAACGAGGAGCGGTGAGCCCATTTGCGCCCAAGCTCT 2399

QY 3430 TAATGAATCGGCCAACCGCGGGGAGAGCGGTTTCGGTATTTCGGCGCTCTTCCGCTTCC 3489
Db 1440 TAATGAATCGGCCAACCGCGGGGAGAGCGGTTTCGGTATTTCGGCGCTCTTCCGCTTCC 1499
QY 3490 TCGCTCACTGACTCGCTGCGCTCGGTTCGGCTCGCGCGAGCGGTATCAGCTCACTCA 3549
Db 1500 TCGCTCACTGACTCGCTGCGCTCGGTTCGGCTCGCGCGAGCGGTATCAGCTCACTCA 1559
QY 3550 AAGCGGTAATACGGTTATCCACAGAATCAGGGGATAAOCGAGAAAGAAACATGTGAGCA 3609
Db 1560 AAGCGGTAATACGGTTATCCACAGAATCAGGGGATAAOCGAGAAAGAAACATGTGAGCA 1619
QY 3610 AAGCGCAGAAAAGCGCAGAACCGTAAAGAGCGCGCTGCTGGGTTTTCATAGG 3669
Db 1620 AAGGGCAGCAAAAGGCCAGAAACCGTAAAGAGCGCGTGTGCTGGGTTTTCATAGG 1679
QY 3670 CTCGGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
Db 1680 CTCGGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1739
QY 3730 ACAGGACTATAAGATAACAGGCGTTTCCCTTGAAGCTCCCTCGTGGCTCTCTGTT 3789
Db 1740 ACAGGACTATAAGATAACAGGCGTTTCCCTTGAAGCTCCCTCGTGGCTCTCTGTT 1799
QY 3790 CCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGGAAGCGTGGCGTT 3849
Db 1800 CCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGGAAGCGTGGCGTT 1859
QY 3850 TCTCATAGCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGTCTCGCTCCAGCTGGGC 3909
Db 1860 TCTCATAGCTCA GCTGTAGGTATCTCAGTTTCGGTGTAGTCTCGCTCCAGCTGGGC 1919
QY 3910 TGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGGTAACTATCGTCTT 3969
Db 1920 TGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGGTAACTATCGTCTT 1979
QY 3970 GAGTCCAAACCGGTAGACACGACTTATCGCCTGCGCAGCAGCCACTGTGTACAGATT 4029
Db 1980 GAGTCCAAACCGGTAGACACGACTTATCGCCTGCGCAGCAGCCACTGTGTACAGATT 2039
QY 4030 AGCAGAGCAGGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCTTAACTACGGC 4089
Db 2040 AGCAGAGCAGGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCTTAACTACGGC 2099
QY 4090 TACA CTAGAAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTCTCGGAAA 4149
Db 2100 TACA CTAGAAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTCTCGGAAA 2159
QY 4150 AGAGTTGGTAGCTCTTGATCGGGCAACAAACCCGCTGGTAGCGGTGTTTTTGT 4209
Db 2160 AGAGTTGGTAGCTCTTGATCGGGCAACAAACCCGCTGGTAGCGGTGTTTTTGT 2219
QY 4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTCTTTGATCTTTCT 4269
Db 2220 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTCTTTGATCTTTCT 2279
QY 4270 ACGGGTCTCAGCTCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGGATCGCGTCGAA 4329
Db 2280 ACGGGTCTCAGCTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAAGCGGATCGCGTCGAA 2339
QY 4330 TCGGAGCGGCGATACCGTTAAGCAGCAGGAAGGGTCAAGCCATTCGCGCCCAAGCTCT 4389
Db 2340 TCGGAGCGGCGATACCGTTAAGCAGCAGGAAGGGTCAAGCCATTCGCGCCCAAGCTCT 2399
QY 4390 TCAGCAATATCACGGGTAGCCAGCTATGCTCTGATAGCGGTCCGCGCACACCCAGCCGG 4449
Db 2400 TCAGCAATATCACGGGTAGCCAGCTATGCTCTGATAGCGGTCCGCGCACACCCAGCCGG 2459
QY 4450 CCA CAGTCGATGAATTCAGAAAAAGCGCCATTTTCCACCATGATATTTGGCGAAGCAGGCA 4509
Db 2460 CCA CAGTCGATGAATTCAGAAAAAGCGCCATTTTCCACCATGATATTTGGCGAAGCAGGCA 2519

QY 4510 TCGCCATGGGTCAACGACGAGATCTTCGCGTGGGCGATCGCGCCTTGAGCCTTGGCGAAC 4569
Db 2520 TCGCCATGGGTCAACGACGAGATCTTCGCGTGGGCGATCGCGCCTTGAGCCTTGGCGAAC 2579
QY 4570 AGTTCCGCTGGCGCGAGCCCTTGATGCTCTTCGTCCAGATCATCTCTGATCGAACAAGCCG 4629
Db 2580 AGTTCCGCTGGCGCGAGCCCTTGATGCTCTTCGTCCAGATCATCTCTGATCGAACAAGCCG 2639
QY 4630 GCTTCATCCGAGTAGTGTCTCGCTCGATCGGATGTTTCGCTGGTGGTTCGATGGGCGAG 4689
Db 2640 GCTTCATCCGAGTAGTGTCTCGCTCGATGCGATGTTTCGCTGGTGGTTCGATGGGCGAG 2699
QY 4690 GTAGCCGATCAAGCGGTATGACGCCCGCATTCGATCAAGCCATGATGATATCTTCTCG 4749
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QY 4750 GCAGGAGCAAGGTGAGATGACGAGAGATCCTGCCCCGGCACTTTCGCCCAATAGAGCCAG 4809
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Db 3000 CCGATTTCTGTTGTCGCCAGTCATAGCCGATAGCTCTCCACCCCAAGCGCGCGAGAA 3059
QY 5050 CTTGCGTCAATCCATCTTGTTCATATCATGCGAAACGATCCTCATCTCTCTTGATCA 5109
Db 3060 CTTGCGTCAATCCATCTTGTTCATATCATGCGAAACGATCCTCATCTCTCTTGATCA 3119
QY 5110 GATCTTTGATCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 5169
Db 3120 GATCTTTGATCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG 3179
QY 5170 CAGGGCTTCCCAACCTTA CAGAGGGGCGCCCGCTGCGCAATTCGCTTCTGCTGCTC 5229
Db 3180 CAGGGCTTCCCAACCTTA CAGAGGGGCGCCCGCTGCGCAATTCGCTTCTGCTGCTC 3239
QY 5230 CATAAAAACCGCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTTGGGGCTCTTCGCTA 5289
Db 3240 CATAAAAACCGCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTTGGGGCTCTTCGCTA 3299
QY 5290 TTAAGCCAGTGGCGAAAGGGGATGCTGCAAGCGGATTAAGTTGGGTAAACGCCAGGG 5349
Db 3300 TTAAGCCAGTGGCGAAAGGGGATGCTGCTGCAAGCGGATTAAGTTGGGTAAACGCCAGGG 3359
QY 5350 TTTTCCAGTCAAGCTTTGTAACGACGCGCAGTGAATTTGTAATACGACTCACTATAG 5409
Db 3360 TTTTCCAGTCAAGCTTTGTAACGACGCGCAGTGAATTTGTAATACGACTCACTATAG 3419
QY 5410 GCGCAATT 5417
Db 3420 GCGCAATT 3427

RESULT 12

ABQ78294

ID ABQ78294 standard; DNA; 2192 BP.

XX

AC ABQ78294;

XX

DT 05-NOV-2002 (first entry)

XX

DE Nucleotide sequence of plasmid pVC0289.

KW Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass;

KW Insulin-like Growth Factor-I; IGF-I; milk production; feed efficiency;

KW somatotroph; growth-related disorder; hypopituitary dwarfism;

KW meat production; egg production; ss.

XX Synthetic.

XX WO200261037-A2.

XX 08-AUG-2002.

XX 12-DEC-2001; 2001WO-US048726.

XX 12-DEC-2000; 2000US-0255021P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX (ADVI-) ADVISYS.

XX Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;

XX WPI; 2002-619237/66.

XX Improving or enhancing growth, lean body mass, milk production, feed

PT efficiency or Insulin-like Growth Factor-I levels, comprises introducing

PT a vector encoding a growth hormone releasing hormone into an animal

PT before or during gestation.

XX Example 2; Page 111-112; 113pp; English.

XX The present sequence represents plasmid pVC0289, which was used to create

CC a vector carrying cDNA encoding pig growth hormone releasing hormone

CC (GHRH) cDNA. Nucleic acids encoding GHRH are used in the method of the

CC invention. The specification describes a method for improving or

CC enhancing characteristics e.g. growth, lean body mass, insulin-like

CC Growth factor (IGF)-I levels, growth rate and milk production in an

CC offspring, and for delaying birth of an offspring. The method comprises

CC introducing a vector, encoding GHRH, into cells of the female animal

CC prior to or during gestation of the offspring under conditions where the

CC nucleotide sequence is expressed. The method is useful of improving or

CC enhancing animal growth, for increasing growth hormone, lean body mass,

CC IGF-I levels, feed efficiency, growth rate, ratio of somatotrophs to

CC other hormone-producing cells in a pituitary gland, and milk production

CC in an offspring, and for delaying birth of an offspring. GHRH nucleic

CC acids and vectors are used for diagnostic purposes in clinical medicine.

CC both human and veterinary, e.g. in treating growth-related disorders such

CC as hypopituitary dwarfism resulting from abnormalities in growth hormone

CC production, and in stimulating the growth and enhancing feed conversion

CC efficiency of animals raised for meat, milk and egg production

XX SQ Sequence 2192 BP; 486 A; 534 C; 601 G; 471 T; 0 U; 0 Other;

Query Match 39.8%; Score 2160; DB 6; Length 2192;

Best Local Similarity 99.5%; Pred. No. 1.1e-268;

Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3190 GAGCCAGGGAACAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAATTCAGCTTGGCG 3249

DB 17 GAGGGGGGGCCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAATTCAGCTTGGCG 76

QY 3250 TAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAAC 3309

DB 77 TAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAAC 136

QY 3310 ATACGAGCCGGAGCAATAAGTGTAAAGCTTGGGGTGCCTTAATGAGTGAGCTAACTCACA 3369

DB 137 ATACGAGCCGGAGCAATAAGTGTAAAGCTTGGGGTGCCTTAATGAGTGAGCTAACTCACA 196

QY 3370 TTAATTCGCTTGGCTCAGCTGCGCGCTTTTCAGTCGGGAAACCTTGTGCGCAGCTGCAT 3429

DB 197 TTAATTCGCTTGGCTCAGCTGCGCGCTTTTCAGTCGGGAAACCTTGTGCGCAGCTGCAT 256

QY 3430 TAATGAATCGGCAACGCGCGGGAGAGCGGTTTCGTATTTGGCGCTCTTTCGCTTCC 3489

DB 257 TAATGAATCGGCAACGCGCGGGAGAGCGGTTTCGTATTTGGCGCTCTTTCGCTTCC 316

QY 3490 TCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCA 3549

DB 317 TCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCA 376

QY 3550 AAGGCGGTATATACGGTTTATCCAGAAATCAGGGGATAACACGAGAAACATGTGAGCA 3609

DB 377 AAGGCGGTATATACGGTTTATCCAGAAATCAGGGGATAACACGAGAAACATGTGAGCA 436

QY 3610 AAAGGCGAGAAAAGGCGAGAAACCGTAAAGAGGCGCGTTCGTGCGGTTTTTTCATAGG 3669

DB 437 AAAGGCGAGAAAAGGCGAGAAACCGTAAAGAGGCGCGTTCGTGCGGTTTTTTCATAGG 496

QY 3670 CTCGCGCCCTCAGCAGGATCACAATAATCAGAGCTCAAGTCAGAGGTGCGGAAACCG 3729

DB 497 CTCGCGCCCTCAGCAGGATCACAATAATCAGAGCTCAAGTCAGAGGTGCGGAAACCG 556

QY 3730 ACAGGACTATAAAGATACACAGGCGTTTCCCTCTGGAAGCTCCCTCGTGGCTCTCTCTGTT 3789

DB 557 ACAGGACTATAAAGATACACAGGCGTTTCCCTCTGGAAGCTCCCTCGTGGCTCTCTCTGTT 616

QY 3790 CCACCTCGCGCTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGCTT 3849

DB 617 CCACCTCGCGCTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGCTT 676

QY 3850 TCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGCTCAAGCTGGGC 3909

DB 677 TCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGCTCAAGCTGGGC 736

QY 3910 TGTGTGCACGAACCCCGCTTACGCGCGCTTACGCGCTTATCCCGTAACTATCGCTT 3969

DB 737 TGTGTGCACGAACCCCGCTTACGCGCGCTTACGCGCTTATCCCGTAACTATCGCTT 796

QY 3970 GAGTCAACCCCGGTAAAGACACGCTTATCCGCTCTGCTGAAGCCAGTACCTTCGGA 4039

DB 797 GAGTCAACCCCGGTAAAGACACGCTTATCCGCTCTGCTGAAGCCAGTACCTTCGGA 856

QY 4030 AGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCGAGTGTGGTGGCTTAACAGCGC 4089

DB 857 AGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCGAGTGTGGTGGCTTAACAGCGC 916

QY 4090 TACACTAGAGAACAGTATTTGTATCTGCGCTCTGCTGAAGCCAGTACCTTCGGA 4149

DB 917 TACACTAGAGAACAGTATTTGTATCTGCGCTCTGCTGAAGCCAGTACCTTCGGA 976

QY 4150 AGAGTTGGTAGCTCTTTGATCCGCAACCAACCCGCTGCTAGCGGTGGTTTTTTTGT 4209

DB 977 AGAGTTGGTAGCTCTTTGATCCGCAACCAACCCGCTGCTAGCGGTGGTTTTTTTGT 1036

QY 4210 TGCAAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAAATCTTTTGATCTTTTCT 4269

DB 1037 TGCAAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAAATCTTTTGATCTTTTCT 1096

QY 4270 ACCGGTCTGACGCTCAGAGAACTCTCAAGAGGCGATAGAGGCGATGCGCTCGAA 4329

DB 1097 ACCGGTCTGACGCTCAGAGAACTCTCAAGAGGCGATAGAGGCGATGCGCTCGAA 1156

QY 4330 TCGGAGCGCGATACCGTAAAGCAGAGAGCGGTTCAGCCCATTCGCCGCCAAGCTCT 4389

DB 1157 TCGGAGCGCGATACCGTAAAGCAGAGAGCGGTTCAGCCCATTCGCCGCCAAGCTCT 1216

QY 4390 TCAGCAATATCACGGTAGCCAAAGCTATGTCTGTATAGCGTCCGCAACCCAGCGG 4449

DB 1217 TCAGCAATATCACGGTAGCCAAAGCTATGTCTGTATAGCGTCCGCAACCCAGCGG 1276

QY 4450 CCACAGTCAGTGAATCCAGAAAGCGCCATTTTCCACCATGATATTCGCGCAGAGGCA 4509

DB 1277 CCACAGTCAGTGAATCCAGAAAGCGCCATTTTCCACCATGATATTCGCGCAGAGGCA 1336

QY 4510 TCGCCATGGTCAACGACGAGATCTCTCGCGCTCGGGCATGCGCGCTTGAGCCTGGCGAAC 4569

XX 19-JUN-2003.
XX 10-DEC-2002; 2002WO-US039509.
XX 11-DEC-2001; 2001US-0339610P.
XX (ADVI-) ADVISYS INC.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
XX Hahn K, Brenner MK;
XX WPI; 2003-558968/52.
XX Treating anemia, immune dysfunction, tumor, increasing total red blood
XX cell mass, reversing wasting or abnormal weight loss in subject, by
XX administering nucleic acid construct encoding growth-hormone-releasing-
XX hormone.
XX Claim 4; Page 193-195; 212pp; English.
XX The invention relates to compositions and methods for plasmid-mediated
XX supplementation. The method is useful for treating anaemia, tumour (such
XX as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
XX dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
XX kidney failure, for preventing the development of metastatic tumour, for
XX increasing total red blood cell mass, for reversing wasting, abnormal
XX weight loss or suppression of lymphopoiesis, in a subject, or for
XX increasing weight gain in a chronically ill subject or, or for extending
XX life expectancy for a chronically ill subject. The present sequence is TV
XX -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
XX used to illustrate the method of the invention
XX SQ Sequence 3534 BP; 764 A; 1016 C; 979 G; 775 T; 0 U; 0 Other;
Query Match 39.8%; Score 2160; DB 9; Length 3534;
Best Local Similarity 99.5%; Pred. No. 1e-268;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 3190 GAGCCAGGACAAAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG 3249
DB 1359 GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG 1418
QY 3250 TAATCATGGTCATAGCTGTTTCCCTGTGTGAATTTATTCGGCTCACAATTCACACAAC 3309
DB 1419 TAATCATGGTCATAGCTGTTTCCCTGTGTGAATTTATTCGGCTCACAATTTCCACAAC 1478
QY 3310 ATACGAGCCGGAAGCATAAGGTAAAGCCCTGGGGTGCCTAATCAGTGAGCTAACTCACA 3369
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QY 3370 TTAATTTGGTTTGGCTCACACTCCCGCTTTTCAGTTCGGGAAACCTGTGTGCGAGCTGCAT 3429
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QY 3550 AAGCGCGTAAATACGGTTATTCACAGAATCAGGGGATTAACGAGGAAAGAAACATGTGAGCA 3609
DB 1719 AAGCGCGTAAATACGGTTATTCACAGAATCAGGGGATTAACGAGGAAAGAAACATGTGAGCA 1778
QY 3610 AAAGCCGAGAAAAGGCCAGGAAACGTTAAAGGCGGGTGTCTGGCGTTTTCATAGG 3669
DB 1779 AAAGCCGAGAAAAGGCCAGGAAACGTTAAAGGCGGGTGTCTGGCGTTTTCATAGG 1838
QY 3670 CTCCGCCCCCTGAGCAGCATCACAAAATTCAGCTCAAAGTTCAGAGGTGGCGAAACCCG 3729

DB 1839 CTCCGCCCCCTGAGCAGCATCACAAAATTCAGCTCAAAGTTCAGAGGTGGCGAAACCCG 1898
QY 3730 ACAGGACTATAAGATACCAAGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTT 3789
DB 1899 ACAGGACTATAAGATACCAAGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTT 1958
QY 3790 CCGACCTCGCGCTTACCGGATACCTGTTCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
DB 1959 CCGACCTCGCGCTTACCGGATACCTGTTCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018
QY 3850 TCTCATAGTTCACGCTGTAGGTATCTCAGTTTCGGTGTAGTGTCTCTCAAGCTCGGC 3909
DB 2019 TCTCATAGTTCACGCTGTAGGTATCTCAGTTTCGGTGTAGTGTCTCTCTCAAGCTCGGC 2078
QY 3910 TGTGTGACGAAACCCCGTTTCAGCCGCGCTTCGGCTTATCCCGTAACTACTCGTCTT 3969
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DB 2859 GTAGCCGATCAAGCGTATGCGCGCGCATTCGATCAGCCATGATGATGATCTTTCTCG 2918
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3	987.2	18.2	1076	1	AU081137	AU081137
4	959	17.7	1089	1	AU081124	AU081124
5	903.2	16.7	1049	10	CL021189	CH216-8A
6	901	16.6	925	6	CB686151	CB686151
7	893.2	16.5	1191	8	DR045882	FP-11_A09
8	859.2	15.8	885	10	CL076016	CH216-13
9	853	15.7	1195	8	DR046031	FP-8_F02.
10	852.8	15.7	951	8	CX983341	UMC_bof_0
11	852.6	15.7	875	8	CX012952	io62d127.b
12	835.6	15.4	1073	6	CF269652	CF269652
13	824.4	15.2	1169	10	AG332951	Mus_muscul
14	823.2	15.2	1025	10	CL021193	CH216-8A
15	820.4	15.1	1163	1	AU081044	AU081044
16	818.8	15.1	868	8	CX984340	UMC_bov_0
17	812.6	15.0	935	7	CK284786	EST747508
18	804.8	14.8	833	6	CB686421	En01b_04j
19	803.6	14.8	966	9	BZ570738	msH2_1513
20	800.4	14.8	804	8	CX979032	UMC_bemiv
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ACCESSION CX943193
VERSION CX943193.1 GI:58802440
KEYWORDS EST.
SOURCE Laminaria japonica
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ORGANISM Laminaria japonica
Eukaryota; stramenopiles; Phaeophyceae; Laminariales;
Laminariaceae; Laminaria.
REFERENCE 1 (bases 1 to 1176)
AUTHORS Xuan,J., Zhao,G., Wang,W., Duan,D., Weng,M. and Wang,B.
TITLE Expressed sequence tag analysis of the brown alga Laminaria
japonica (Phaeophyceae)
JOURNAL Unpublished (2005)
COMMENT Contact: Xuan JS
The State Key Laboratory of Plant Genome Research
Institute of Genetics and Developmental Biology, Chinese Academy of
Science
Datun Road, Chaoyang District, Beijing, China, 100101
Tel: 086 010 64889353
Fax: 086 010 64873428
Email: bnxuan@hotmail.com
Seq primer: T3 Forward
High quality sequence stop: 1176.
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/clone_lib="Laminaria japonica Lambda Zap Express Library"
/note="Vector: Uni-ZAP@ XR vector; Site_1: EcoRI; Site_2:
XhoI"
ORIGIN
Query Match 18.3%; Score 992.4; DB 8; Length 1176;
Best Local Similarity 99.0%; Pred. No. 2.2e-272;
Matches 1030; Conservative 0; Mismatches 6; Indels 4; Gaps 3;
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Db 37 CGTAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACACA 96
Qy 3308 ACATACGAGCGGAACATAAGGTAAAGCCTGGGGTGCTTAATGAGTGAGCTAACTCA 3367
Db 97 ACATACGAGCGGAACATAAGGTAAAGCCTGGGGTGCTTAATGAGTGAGCTAACTCA 156
Qy 3368 CATTAAATGCGTTCGCTCACTGCCGCTTTTCCAGTCGGGAACCTGTGCTGCGAGCTGC 3427
Db 157 CATTAAATGCGTTCGCTCACTGCCGCTTTTCCAGTCGGGAACCTGTGCTGCGAGCTGC 216
Qy 3428 ATTAATGAATCGGCACAAACGCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTT 3487
Db 217 ATTAATGAATCGGCACAAACGCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTT 276
Qy 3488 CCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCACT 3547
Db 277 CCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCACT 336
Qy 3548 CAAAGGCGGTAATACCGTTCATCCAGAAATCAGGGGATACCGAGGAAGAAACATGTGAG 3607
Db 337 CAAAGGCGGTAATACCGTTCATCCAGAAATCAGGGGATACCGAGGAAGAAACATGTGAG 396
Qy 3608 CAAAGGCGGTAATACCGGTAATCCGTAAGAAAGCGCGGTTGCTGGCGCTTTTCCATA 3667
Db 397 CAAAGGCGGTAATACCGGTAATCCGTAAGAAAGCGCGGTTGCTGGCGCTTTTCCATA 456
Qy 3668 GGCTCCGCCCTCGAGCATCACAAAATCGAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 3727
Db 457 GGCTCCGCCCTCGAGCATCACAAAATCGAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 516
Qy 3728 CGACGAGACTATAAGATACCGGCTTTTCCCTCGGAAGCTCCCTCGTGGCTCTCCTG 3787
Db 517 CGACGAGACTATAAGATACCGGCTTTTCCCTCGGAAGCTCCCTCGTGGCTCTCCTG 576
Qy 3788 TTCCGACCTCGCGCTTACCGGATACCTGTGCGCTTTCCTTCCCTTCCGGAAGGTCGCGC 3847
Db 577 TTCCGACCTCGCGCTTACCGGATACCTGTGCGCTTTCCTTCCCTTCCGGAAGGTCGCGC 636
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Db 1064 GC GC 1067

RESULT 4
AU081124 1089 bp mRNA linear EST 30-JUL-2002
LOCUS AU081124 Oncorhynchus mykiss Kidney infected by infectious
DEFINITION hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KG/12,
mRNA sequence.
ACCESSION AU081124 GI:6431472
VERSION AU081124.1
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 1089)
REFERENCE Kono,T., Sakai,M. and LaPatra,S.E.
AUTHORS Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
TITLE Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT Contact: Masahiro Sakai
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES
Source
1. 1089
Location/Qualifiers
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="KG/12"
/tissue_type="kidney"
/clone_lib="Oncorhynchus mykiss Kidney infected by
infectious hematopoietic necrosis virus"
/notes="common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"
ORIGIN

Query Match 17.7%; Score 959; DB 1; Length 1089;
Best Local Similarity 97.5%; Pred. No. 8.2e-263;
Matches 1017; Conservative 0; Mismatches 20; Indels 6; Gaps 4;

QY 3207 CAGCTTTTGTCCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATGGTCATAGCT 3266
DB 47 CAGCTTTTGTCCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATGGTCATAGCT 106
QY 3267 GTTTCCTGTGTGAATTTGTTATCCGCTCACAATTTCCACACATACGAGCCGGAAGCAT 3326
DB 107 GTTTCCTGTGTGAATTTGTTATCCGCTCACAATTTCCACACATACGAGCCGGAAGCAT 166
QY 3327 AAAGTGAAGCCTGGGGTGCTTAATGAGTGAGTAACTCACAATTAATGGTTGCGCTC 3386
DB 167 AAAGTGAAGCCTGGGGTGCTTAATGAGTGAGTAACTCACAATTAATGGTTGCGCTC 226
QY 3387 ACTGCCGCTTTCAGTTCGGGAAACCTGTGTCGACGTGATTAATGAATTCGGCCAAAG 3446
DB 227 ACTGCCGCTTTCAGTTCGGGAAACCTGTGTCGACGTGATTAATGAATTCGGCCAAAG 286
QY 3447 CGCGGGAGAGCGGTTTGGTATTTGGCGGCTTTCGCTTCCCTCACTGACTCGCT 3506
DB 287 CGCGGGAGAGCGGTTTGGTATTTGGCGGCTTTCGCTTCCCTCACTGACTCGCT 346
QY 3507 GCGCTCGCTTTCGCTTGGCGGAGCGGTATCAGCTCAGTCAAAAGCGGTAATACGGTT 3566
DB 347 GCGCTCGCTTTCGCTTGGCGGAGCGGTATCAGCTCAGTCAAAAGCGGTAATACGGTT 406
QY 3567 ATCCACAGATTCAGGGGATACCGCAGGAAAGAAATGTGAGCAAAAGCCAGCAAAAGGC 3626
DB 407 ATCCACAGATTCAGGGGATACCGCAGGAAAGAAATGTGAGCAAAAGCCAGCAAAAGGC 466
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3627 CAGGAACCGTAAAGGCGCGGTGCTGGCGTTTTCCATAGGCTCGCCCCCTGACGA 3686
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467 CAGGAACCGTAAAGGCGCGGTGCTGGCGTTTTCCATAGGCTCGCCCCCTGACGA 526
|||||
3687 GCATCAAAAATCGAGGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATA 3746
|||||
527 GCATCAAAAATCGAGGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATA 586
|||||
3747 CCAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCGCTCTCCCTGTTCCGACCTGCGGCTTAC 3806
|||||
587 CCAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCGCTCTCCCTGTTCCGACCTGCGGCTTAC 646
|||||
3807 CGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 3866
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647 CGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG 706
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3867 TAGGTATCTCAGTTCGGTGTAGTGTGCTCTCAAGCTGGCGCTGTGTGACGAACCCCG 3926
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707 TAGGTATCTCAGTTCGGTGTAGTGTGCTCTCAAGCTGGCGCTGTGTGACGAACCCCG 766
|||||
3927 CGTTCAGCGCGACCGCTGGCGCTTATCCGCTAACTATCGTCTTGAAGTCCAAACCGGTAAG 3986
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767 CGTTCAGCGCGACCGCTGGCGCTTATCCGCTAACTATCGTCTTGAAGTCCAAACCGGTAAG 826
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3987 ACACGACTTATCGCCACTGCGCAGCAGCACTGGTAAACAGGATTAGCAGAGCGAGTATGT 4046
|||||
827 ACACGACTTATCGCCACTGCGCAGCAGCACTGGTAAACAGGATTAGCAGAGCGAGTATGT 886
|||||
4047 AGCGGCTGTACAGAGTCTTGAAG-TGGTGGCTTAACCTACGCTACACTAGAAGAACAG 4105
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887 AGCGGCTGTACAGAGTCTTGAAGTGTGTGGCTTAACTACGCTACACTAGAAGAACAG 946
|||||
4106 TATTTGGTATCTCGGCTCTGCTGAAGCAGTACCTTCGGAAGGAGGTTGGTAGCTCTT 4165
|||||
947 TATTTGGTATCTCGGCTCTGCTGAAGCAGTACCTTCGGAAGGAGGTTGGTAGCTCTT 1006
|||||
4166 -GATCCGGGCAAAACAAACCA---CCGCTGGTAGGGGTGTTTTTTTGTTCGAAGCA-GCA 4220
|||||
1007 GGATCCGGGCAAAACAAACACCGCTGGGAAGGGGGGTGCTCTTTTGTTCGAAGCAAGCA 1066
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4221 GATTACGCGCAGAAACAAAGGAT 4243
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1067 GATTACGCGCAGAAACAAACCGAT 1089
|||||

RESULT 5
CL021189 1049 bp DNA linear GSS 31-DEC-2003
LOCUS CH216-8A14 RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A14,
DEFINITION genomic survey sequence.
ACCESSION CL021189
VERSION CL021189.1 GI:40463002
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 1049)
REFERENCE Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
AUTHORS Mardis,E. and Wilson,R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TAGCACTCACTATAGGAGA
Class: BAC ends
High quality sequence start: 43
High quality sequence stop: 888.
Location/Qualifiers

FEATURES
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source 1.1049
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-8A14"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN
Query Match 16.7%; Score 903.2; DB 10; Length 1049;
Best Local Similarity 98.4%; Pred. No. 8.5e-247;
Matches 933; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 3237 TTGAGCTTGGCGTAATCATGTCATAGCTGTTTCTGTGTGAAATTTATTCGGCTCAC 3296
DB 101 TGCAGCTTGGCGTAATCATGTCATAGCTGTTTCTGTGTGAAATTTATTCGGCTCAC 160

QY 3297 AATTCCACACATACGAGCGGAGCATAAAGTGTAAAGCTCGGGTGCCCTAATGAGT 3356
DB 161 AATTCCACACATACGAGCGGAGCATAAAGTGTAAAGCTCGGGTGCCCTAATGAGT 220

QY 3357 GAGCTAACTCACAATTAATGCGTTGCGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTC 3416
DB 221 GAGCTAACTCACAATTAATGCGTTGCGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTC 280

QY 3417 GTGCCAGCTGCATTAATGAAATCGGCCAAGCGCGGGGAGAGCGGTTTGGCTAATGGCG 3476
DB 281 GTGCCAGCTGCATTAATGAAATCGGCCAAGCGCGGGGAGAGCGGTTTGGCTAATGGCG 340

QY 3477 CTCTTCGGCTTCTCGCTCACTCACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 3536
DB 341 CTCTTCGGCTTCTCGCTCACTCACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 400

QY 3537 ATCAGCTCACTCAAAGCGGTAATACGGTTTATCCACAGATCAGGGGATAAACGAGGAA 3596
DB 401 ATCAGCTCACTCAAAGCGGTAATACGGTTTATCCACAGATCAGGGGATAAACGAGGAA 460

QY 3597 GAACATGTGAGCAAAAGCGCAGCAAAAGCGCAGGAAACCGTAAAGAGCGCGTGTGCTGC 3656
DB 461 GAACATGTGAGCAAAAGCGCAGCAAAAGCGCAGGAAACCGTAAAGAGCGCGTGTGCTGC 520

QY 3657 GTTTTTCATAGGCTCGCCCTCGAGGATCAAAAATCGAGCTCAAGTCAGAG 3716
DB 521 GTTTTTCATAGGCTCGCCCTCGAGGATCAAAAATCGAGCTCAAGTCAGAG 580

QY 3717 GTGGGAAACCCGACAGGACTATAAGATACAGAGCGTTTCCCGCTGGAAGCTCCCTCGT 3776
DB 581 GTGGGAAACCCGACAGGACTATAAGATACAGAGCGTTTCCCGCTGGAAGCTCCCTCGT 640

QY 3777 GGGCTCTCTGTTCCAGCTCGCTTACCGGATACCTGTGCGCTTCTTCCCTTCGGG 3836
DB 641 GGGCTCTCTGTTCCAGCTCGCTTACCGGATACCTGTGCGCTTCTTCCCTTCGGG 700

QY 3837 AAGCTGGCGCTTCTCATAGCTCAAGCTGTAGTATCTCAGTTCGGTGTAGTGTGCTG 3896
DB 701 AAGCTGGCGCTTCTCATAGCTCAAGCTGTAGTATCTCAGTTCGGTGTAGTGTGCTG 760

QY 3897 CTCGAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCCGAGCGCTGCGCTTATCCGG 3956
DB 761 CTCGAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCCGAGCGCTGCGCTTATCCGG 820

QY 3957 TAACTATCGTTTGTAGTCAACCCCGTAAAGACACGACTTATGCCACTGCGCAGCCAC 4016
DB 821 TAACTATCGTTTGTAGTCAACCCCGTAAAGACACGACTTATGCCACTGCGCAGCCAC 880

QY 4017 TGGTAACAGGATTAGCAGAGCGAGGATGTAGAGCGGTGTCTACAGATTTCTTGAAGTGTG 4076
DB 881 TGGTAACAGGATTAGCAGAGCGAGGATGTAGAGCGGTGTCTACAGATTTCTTGAAGTGTG 940

QY 4077 GCCTAACTACGGCTACACTAGAGAAC-AGTATTTGTATCTCGCTCTCTGCTGAGCCAG 4135
DB 941 GCCTAACTACGGCTACACTAGAGAACAGTATTTGTATCTCGCTCTCTGCTGAGCCAG 1000

QY 4136 TTACC-TTCGGAAGAGTTGCTAGCTCTTGATCCGGCAACAAACC 4182
DB 1001 TTACC-TTCGGAAGAGTTGCTAGCTCTTGATCCGGCAACAAACC 1048

RESULT 6
CB686151/c 925 bp mRNA linear EST 09-APR-2003
LOCUS Bn01b_02008 A
DEFINITION Bn01b AAFPC ECORC transgenic Brassica napus overexpressing BNCBF17 c
onstitutively_frost_tolerant Brassica napus cDNA clone Bn01b_02008,
mRNA sequence.
ACCESSION CB686151 GI:29689876
VERSION CB686151.1
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 925)
AUTHORS Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,
Chagnon, J., Farah, S., Couroux, P. and Hattori, J.
TITLE Expressed Sequence Tags from constitutively frost tolerant
transgenic Brassica napus overexpressing BNCBF17
JOURNAL Unpublished (2002)
COMMENT Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@agr.gc.ca.

FEATURES
source
1..925
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Westar"
/db_xref="taxon:3708"
/clone="Bn01b_02008"
/tissue_type="fourth leaf"
/dev_stage="3 weeks seedling grown at room temperature"
/clone_lib="Bn01b AAFPC ECORC transgenic Brassica napus_ove
rexpressing BNCBF17 constitutively frost tolerant"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
Site 2: XhoI; Germinated in soil flats and seedlings grown
for 3 weeks in a Conviron B-15 cabinet set at 20°C/16 hr
light (250 Em-2sec-1) and 16 °C/ 8 hr dark. Fourth leaves
collected at 9 am and immediately frozen."

ORIGIN
Query Match 16.6%; Score 901; DB 6; Length 925;
Best Local Similarity 98.6%; Pred. No. 3.5e-246;
Matches 912; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 3212 TTTGTTCCCTTTAGTGAGGTTAAATTCGAGCTTGGCGTAATCATGCTCATAGCTGTTTC 3271
DB 924 TTTGTTCCCTTTAGTGAGGTTAAATTCGCGCTTGGCGTAATCATGCTCATAGCTGTTT - 866

QY 3272 CTGTGTGAATTTGTTATCCGCTCAAAATTCACAAACATACAGCCGGAAGCATAAAGT 3331
DB 865 CTGTGTGAATTTGTTATCCGCTCAAAATTCACAAACATACAGCCGGAAGCATAAAGT 806

QY 3332 GTAAAGCTCGGGTGCCTTAATGAGTGAAGTAACTCAATTAATTTGCGTCACTGC 3391
DB 805 GTAAAGCTCGGGTGCCTTAATGAGTGAAGTAACTCAATTAATTTGCGTCACTGC 746

QY 3392 CGCTTTTCAGTCGGGAAACCTGTCTGTCAGCTGATTAATGAATCGGCAACGCGCG 3451
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Db 745 CCGCTTCCAGTCGGGAACCTGTCGTGCCAGTCGATTAATGAATCGGCAACGCGCG 686
Qy 3452 GGAGAGCGGTTGGCGTATTTGGCGCTCTTCGCGCTTCCTCGCTCACTGACTCGCTCGCT 3511
Db 685 GGAGAGCGGTTGGCGTATTTGGCGCTCTTCGCGCTTCCTCGCTCACTGACTCGCTCGCT 626
Qy 3512 CGGTGCTCGGCTGCGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCA 3571
Db 625 CGGTGCTCGGCTGCGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCA 566
Qy 3572 CAGAATCAGGGGATAACGCAAGGAAGAA CATGTGAGCAAAAGCCAGCAAAAGCCAGGA 3631
Db 565 CAGAATCAGGGGATAACGCAAGGAAGAA CATGTGAGCAAAAGCCAGCAAAAGCCAGGA 506
Qy 3632 ACCGTAAAAGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCGCCCTCGTACGAGATC 3691
Db 505 ACCGTAAAAGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCGCCCTCGTACGAGATC 446
Qy 3692 ACAAATCAGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGACTATTAAGATACAGG 3751
Db 445 ACAAATCAGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGACTATTAAGATACAGG 386
Qy 3752 CGTTTCCCTGGAAGCTCCCTGCTGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGAT 3811
Db 385 CGTTTCCCTGGAAGCTCCCTGCTGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGAT 326
Qy 3812 ACTGTCCGCTTTCCTCCCTTCGGGAAGCGTGCGCTTCTCATAGTCACTGCTAGGT 3871
Db 325 ACTGTCCGCTTTCCTCCCTTCGGGAAGCGTGCGCTTCTCATAGTCACTGCTAGGT 266
Qy 3872 ATCTCAGTTCCGTTAGGTGCTTCCCTCCAGCTGGGCTGTGTGACAGAACCCCGCTTC 3931
Db 265 ATCTCAGTTCCGTTAGGTGCTTCCCTCCAGCTGGGCTGTGTGACAGAACCCCGCTTC 206
Qy 3932 AGCCGACCGCTGCGCTTATCCGTTAACTATGCTCTTGAGTCCAAACCCGTTAAGACAG 3991
Db 205 AGCCGACCGCTGCGCTTATCCGTTAACTATGCTCTTGAGTCCAAACCCGTTAAGACAG 146
Qy 3992 ACTTATCGCCACTGGCAGCAGCACTGGTAACAGGATTAGCAGAGGAGGTATGTAGCG 4051
Db 145 ACTTATCGCCACTGGCAGCAGCACTGGTAACAGGATTAGCAGAGGAGGTATGTAGCG 86
Qy 4052 GTGCTACAGATTCTTCAAGTGTGGCTAACTACGCTACACTAGAGAACAGATTTTG 4111
Db 85 GTGCTACAGATTCTTCAAGTGTGGCTAACTACGCTACACTAGAGAACAGATTTTG 26
Qy 4112 GTATCTCGCTCTGCTGAAGCCAGT 4136
Db 25 GTATCTCGCTCTGCTGAAGCCAGT 1

RESULT 7
DR045882
LOCUS
DEFINITION
  PP-11_A09.SEQ cDNA library of Phaeosphaeria nodorum grown on wheat
  cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
ACCESSION
  DR045882
VERSION
  1 (bases 1 to 1191)
KEYWORDS
  EST.
SOURCE
  Phaeosphaeria nodorum
  Phaeosphaeria nodorum
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
  Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
REFERENCE
  1 (bases 1 to 1191)
  Bindaschledler, L.V., Cooper, R.M., Thomas, S.W., Madrid, M.P. and
  Oliver, R.P.
  cDNA library of Phaeosphaeria nodorum grown on wheat cell walls
  unpublished (2005)
  Contact: Richard Oliver
  Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
  Murdoch University
  South Street, Murdoch, W.A 6150, Australia
```

```
Tel: +0893607404
Email: roliver@murdoch.edu.au.
Location/Qualifiers
  1. .1191
  /organism="Phaeosphaeria nodorum"
  /mol_type="mRNA"
  /db_xref="taxon:13684"
  /clone_lib="cDNA library of Phaeosphaeria nodorum grown on
  wheat cell walls"

FEATURES
  source
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Query Match      16.5%; Score 893.2; DB 8; Length 1191;
Best Local Similarity 99.2%; Pred. No. 6.e-244;
Matches 919; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

Qy 3207 CAGCTTTTGTTCCTTTAGTGAGGGTTAATTTTCGAGCTTGGCGTAATCATGTGTCATAGCT 3266
Db 114 CAGCTTTTGTTCCTTTAGTGAGGGTTAATTTTCGAGCTTGGCGTAATCATGTGTCATAGCT 173
Qy 3267 GTTTCCTGTGTAATTTGTTATCCGCTCAAAATTCACACAAATACGAGCCCGAAGCAT 3326
Db 174 GTTTCCTGTGTAATTTGTTATCCGCTCAAAATTCACACAAATACGAGCCCGAAGCAT 233
Qy 3327 AAAAGTGAAGCGCTGGGTCCTTAATGAAGTGAAGTAACTACATTAATTTGCGTTGCGCTC 3386
Db 234 AAAAGTGAAGCGCTGGGTCCTTAATGAAGTGAAGTAACTACATTAATTTGCGTTGCGCTC 293
Qy 3387 ACTGCCGCTTTCAGTTCGGGAACCTTCGTCGAGCTGCATTAATGAATCGGCCAACG 3446
Db 294 ACTGCCGCTTTCAGTTCGGGAACCTTCGTCGAGCTGCATTAATGAATCGGCCAACG 353
Qy 3447 CGCGGGAGAGGCGGTTTGCCTATTCGGGCTCTTCGCTTCCTCGCTCACTGACTCGCT 3506
Db 354 CGCGGGAGAGGCGGTTTGCCTATTCGGGCTCTTCGCTTCCTCGCTCACTGACTCGCT 413
Qy 3507 GCCTCGCTGCTTTCGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTT 3566
Db 414 GCCTCGCTGCTTTCGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTT 473
Qy 3567 ATCCACAGAAATCAGGGGATAACGCAAGGAAGACATGTGAGCAAAAGCCGCAAAAGGC 3626
Db 474 ATCCACAGAAATCAGGGGATAACGCAAGGAAGACATGTGAGCAAAAGCCGCAAAAGGC 533
Qy 3627 CAGGAACCGTAAAGAACGCGCTTTCGCTGCGGCTTTTCCATAGGCTCCGCCCTCGCTACGA 3686
Db 534 CAGGAACCGTAAAGAACGCGCTTTCGCTGCGGCTTTTCCATAGGCTCCGCCCTCGCTACGA 593
Qy 3687 GCATCAAAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 3746
Db 594 GCATCAAAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA 653
Qy 3747 CAGGGGCTTTCCTCCCTGGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTCGCGCTTAC 3806
Db 654 CAGGGGCTTTCCTCCCTGGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTCGCGCTTAC 713
Qy 3807 CGGATACCTGTCGCGCTTTCCTTCGCGGAAGCGTGGCGCTTCTCATAGCTCACGCTG 3866
Db 714 CGGATACCTGTCGCGCTTTCCTTCGCGGAAGCGTGGCGCTTCTCATAGCTCACGCTG 773
Qy 3867 TAGGTATCTCAGTTTCGCTGAGGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCC 3926
Db 774 TAGGTATCTCAGTTTCGCTGAGGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCC 833
Qy 3927 CGTTACGCGCGAGCGCTGCGCTTATTCGGTAACTATTCGTTGAGTCCAAACCCGTTAG 3986
Db 834 CGTTACGCGCGAGCGCTGCGCTTATTCGGTAACTATTCGTTGAGTCCAAACCCGTTAG 893
Qy 3987 ACAGGCTTATCCGCTGCGAGCGCACTGTGTAACAGGATTAGCAGAGCGAGGTATGT 4046
Db 894 ACAGGCTTATCCGCTGCGAGCGCACTGTGTAACAGGATTAGCAGAGCGAGGTATGT 953
Qy 4047 AGCGGCTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTTACACTAGAGAAACAGT 4106
Db 4106 AGCGGCTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTTACACTAGAGAAACAGT 4106
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Db 954 CG--CGTGTACAGAGTTCTTGAAGTGGTGGCTTAACACTACGGGTACACTAGA--GACAGT 1009
QY 4107 ATTGGTATCTGGCTCTGCTGAAGC 4132
Db 1010 ATTGGTATCTGGCTCTGCTGAAGC 1035

RESULT 8
CL076016 885 bp DNA linear GSS 31-DEC-2003
DEFINITION CH216-138F20_RM1.1 CH216 Xenopus tropicalis genomic clone
ACCESSION CH216-138F20, genomic survey sequence.
VERSION CL076016
KEYWORDS CL076016.1 GI:40531929
SOURCE GSS.
ORGANISM Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 885)
AUTHORS Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert length: 175000 Std Error: 0.00
Seq primer: RM1 TAGGACTCACTATAGGAGA
Class: BAC ends
High quality sequence start: 11
High quality sequence stop: 810.
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source Location/Qualifiers
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/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-138F20"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN
Query Match 15.8%; Score 859.2; DB 10; Length 885;
Best Local Similarity 99.4%; Pred. No. 3.4e-234;
Matches 872; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 3280 AATTGTATCGCTCACAAATTCACACACATACGACCGGAGCATAAAGTGTAAAGCC 3339
Db 5 AATTGTATCGCTCACAAATTCACACACATACGACCGGAGCATAAAGTGTAAAGCC 64
QY 3340 TGGGGTGCCCTAATGAGTGAGCTAACTCACATTAATGCGTTGCGCTACCTGCCCGCTTTC 3399
Db 65 TGGGGTGCCCTAATGAGTGAGCTAACTCACATTAATGCGTTGCGCTACCTGCCCGCTTTC 124
QY 3400 CAGTCGGGAAACCTGTGTCGCCAGCTGCATTAAATGAATCGGCCAACCGCGGGGAGAGGC 3459
Db 125 CAGTCGGGAAACCTGTGTCGCCAGCTGCATTAAATGAATCGGCCAACCGCGGGGAGAGGC 184
QY 3460 GGTTCGGTATTTGGGCGCTCTTCGGCTTCCTCGCTACCTGACTCGCTCGCTCGGTCGTT 3519
Db 185 GGTTCGGTATTTGGGCGCTCTTCGGCTTCCTCGCTACCTGACTCGCTCGCTCGGTCGTT 244
QY 3520 CGGCTCGGGGAGCGGTATCAGCTCACTCAAAGCGGTAATCGGTTATCCACAGATCA 3579
Db 245 CGGCTCGGGGAGCGGTATCAGCTCACTCAAAGCGGTAATCGGTTATCCACAGATCA 304
QY 3580 GGGGATAACCGCAGGAAAGAACATGTGAGCAAAAGGGCCAGCAAAAGGCCAGGAACCGGTAAA 3639
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Db 305 GGCGATAACCGCAGGAAAGAACATGTGAGCAAAAGGGCCAGCAAAAGGCCAGTAAC 364
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QY 3700 CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGGCTTTCCC 3759
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QY 3760 CTTGGAGAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC 3819
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QY 3820 GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 3879
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QY 3880 TCGGTGTAGTTCGTTCCGCTCCAGCTGGGCTGTGTGCAGAACCCCGCTTCAGCCCGAC 3939
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QY 3940 CGCTGCGCTTATCCGTTAACTATCTGTGAGTCCAAACCCGTAAGACAGCACTTATCG 3999
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QY 4000 CCACTGGCAGCAGCCACTGTAAACAGATTAGCAGAGCAGGATATGTAGCGGTGTCTACA 4059
Db 725 CCACTGGCAGCAGCCACTGTAAACAGATTAGCAGAGCAGGATATGTAGCGGTGTCTACA 784
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RESULT 9
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LOCUS FP-8 F02.SBQ cDNA library of Phaeosphaeria nodorum grown on wheat
DEFINITION cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
ACCESSION DR046031
VERSION DR046031.1 GI:66909867
KEYWORDS EST.
SOURCE Phaeosphaeria nodorum
ORGANISM Phaeosphaeria nodorum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and
Oliver,R.P.
TITLE cDNA library of Phaeosphaeria nodorum grown on Wheat cell walls
JOURNAL Unpublished (2005)
COMMENT Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.
FEATURES
source Location/Qualifiers
1..1195
/organism="Phaeosphaeria nodorum"
/mol_type="mRNA"
/db_xref="taxon:13684"
/clone_lib="cDNA library of Phaeosphaeria nodorum grown on
wheat cell walls"

ORIGIN
Query Match 15.7%; Score 853; DB 8; Length 1195;
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Best Local Similarity 98.2%; Pred. No. 2.3e-232; Matches 906; Conservative 0; Mismatches 10; Indels 7; Gaps 4;	
QY	3207 CAGCTTTTGTTCCTTTAGTGAGGTTAAATTCGAGCTTGGCGTAAATCATGTCATAGCT 3266
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QY	3327 AAAGTGAACGCTTGGGTCCTAATGAGTGAGCTAACTCACATTAATGCGTTGGCTC 3386
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QY	3507 GCGCTCGGTCGTTGCGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTT 3566
Db	469 GCGCTCGGTCGTTGCGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTT 528
QY	3567 ATCCACAGATCAGGGGATTAACGAGGAAGACATGTGAGCAAAAGCCGCAAAAGGC 3626
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QY	3627 CAGGAACCGTAAAGAGCGGTTGCTGGGCTTTTCCATAGGCTCCGCCCTCGACGA 3686
Db	589 CAGGAACCGTAAAGAGCGGTTGCTGGGCTTTTCCATAGGCTCCGCCCTCGACGA 648
QY	3687 GCATCACAATAATCGACGCTCAAGTCAGAGTGCGGAAACCCGACAGACTATAAAGATA 3746
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Db	709 CCAGGCGTTTCCCTCGAAGCTCCCTGTCGCTCTCCTGTTCCGACCTGCGCTTAC 768
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QY	3867 TAGGTATCTCAGTTTCGGTGTAGGTGCTTCGCTCCAAGTCGGGCTGTGTGACGAAACCCC 3926
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QY	3927 CGTTACGCGCAACGCTGCGCTTATCGGTAACCTATCGTTGAGTCCAAACCGGTAAAG 3986
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QY	3987 ACAGCACTTATCGCCACTGGCAGCAGCACCTGTAACAGGATTACGAGCGAGGTATGT 4046
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QY	4047 AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCGCTACACTAGAAGACAGT 4106
Db	1008 AG--CGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCGCTACACTAGAAGACAGT 1062
QY	4107 ATTTGGTATTCGCGCTCTGCTGA 4129
Db	1063 A-TTGGTATTCGCGCTCTGCTGA 1084

RESULT 10
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LOCUS 951 bp mRNA linear EST 30-NOV-2004
DEFINITION UMC-bof_0A01-002-g06 Ovarian Follicle bof Bos taurus cDNA 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

FEATURES
source

CV983341
CV983341.1 GI:56144062
EST.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 951)
Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
Roberts,R.M., Smith,M.F. and Youngquist,R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
Reproduction
Unpublished (2002)
Contact: DNA Core Facility (Bovine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: bovine@net.missouri.edu
POLYA=No.

Location/Qualifiers
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/mol_type="mRNA"
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/dev_stage="Ovarian Follicle"
/clone_lib="bof"
/note="Vector: pSport1; Funding: The production of ESTs
submitted in this project was funded by USDA Grant
MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female
Reproduction' to RS Prather (Primary Investigator), E
Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF
Smith and RS Youngquist. Genetic Source: Heifers for the
project were purchased from Circle A Ranch, Iberia, MO
(http://www.circlea ranch.com/home.html). These heifers,
while not registered have known Angus pedigrees going back
at least 4 generations. Samples collected: The samples
consisted of the following: germinal vesicle-stage
oocytes; in vitro derived embryos (2-cell, morula,
blastocyst and nuclear transfer blastocyst); in vivo
blastocysts and conceptuses (days 8, 14, 16 and 18);
corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
follicles (days 0, non-recruited, recruited, early
selected and preovulatory); oviduct (days 0, 3 and 5);
endometrium (days 5, 8, 14, 16, 18 and 35); and
placenta/embryo from day 35 conceptuses. Expanded
descriptions of how the tissues were collected can be
found at the following URL:
http://genome.mnet.missouri.edu/Bovine/Methods.html.
Library construction (Standard Protocol): All procedures
have been described in detail elsewhere (Soares et al.,
1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
cellular RNA from each sample was isolated by using
STAT-60 reagent (Tel-Test, Friendswood, TX) and the
poly(A)+ RNA was obtained by two rounds of purification
with the Oligotex mRNA isolation kit (Qiagen) according to
the manufacturer's instructions. The libraries were
constructed essentially as described by the manufacturer's
instructions provided with the SuperScript plasmid system
(Invitrogen, cat. no. 18248-013). Briefly, 1mcg of
poly(A)+ RNA was annealed at c37 degrees with 10mcg of
NotI-tag-dT18 oligonucleotide (GCTGCTCGGCGCGC-tag-T18)
and reverse transcribed at c37 degrees with SuperScript II
(Invitrogen) reverse transcriptase (Jiang et al., 2001).
The 'tag' represents a tissue/stage-specific ten-base
sequence identifier
(http://genome.uiowa.edu/pubsoft/software.html) present in
the oligonucleotide used to prime first-strand synthesis.
Second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis, the double-stranded cDNAs

were ligated to Sali adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and Sali sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dT18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a Sali site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dT oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and Sali and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's group at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Ronaldo MF, Lennon G, Soares MB.. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Estrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG TISSUE=Ovarian Follicle TAG_SEQ=Not found"

ORIGIN

Query Match 15.7%; Score 852.8; DB 8; Length 951;
 Best Local Similarity 99.8%; Pred. No. 2.4e-232;
 Matches 854; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3498 TGACTCGCTCGCTCGCTCGCTCGCGCGAGCGGTATCAGCTCACTCAAGCGGT 3557
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Db 62 TGACTCGCTCGCTCGCTCGCTCGCGCGAGCGGTATCAGCTCACTCAAGCGGT 121
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QY 3558 AATACGGTTATCCACAGATCAGGGGATACGCGAGGAAGACATGTGAGCAAAAGGCCA 3617

Db 122 AATACGGTTATCCACAGATCAGGGGATACGCGAGGAAGACATGTGAGCAAAAGGCCA 181
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QY 3618 GCAAAAGGCCAGGAACCGTAAAGAGCGCGTTTGGCTGGCGTTTTCATAGGCTCGGCC 3677
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Db 182 GCAAAAGGCCAGGAACCGTAAAGAGCGCGTTTGGCTGGCGTTTTCATAGGCTCGGCC 241
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QY 3678 CCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGCGCAAAACCGACAGACT 3737
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Db 242 CCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGCGCAAAACCGACAGACT 301
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QY 3738 ATAAAGATACGAGCGGTTTCCCGCTCGAAGCTCCCTCGTGGCTCTCTGTTCCGACCT 3797
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Db 302 ATAAAGATACGAGCGGTTTCCCGCTCGAAGCTCCCTCGTGGCTCTCTGTTCCGACCT 361
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QY 4098 AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTGGAAAAAGATTGG 4157
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Db 662 AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTGGAAAAAGATTGG 721
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QY 4158 TAGCTCTTATCCGGCAACCAACACCGCTGCTAGCGGTGGTGGTGGTGGTGGTGGTGGTGG 4217
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 ACCESSION CX012952
 VERSION CX012952.1 GI:56395363
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 875)
 AUTHORS Baliya, V.S., Nascimento, L.U. and McCombie, W.R.
 TITLE ESTs from Canis familiaris whole heart (dog)
 JOURNAL Unpublished (2004)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA

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Tel: 516 367 8884
Fax: 516 367 8874
Email: mcmombie@csli.org.
Location/Qualifiers
1. .875
/organism="Canis familiaris"
/mol_type="mRNA"
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/dev_stage="3 month old normal canine"
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/clone_lib="Whole Heart Library (DOGESTS)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site 1:
EcoRI; Site 2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Hawkins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

FEATURES             source
Query Match          15.7%; Score 852.6; DB 8; Length 875;
Best Local Similarity 99.0%; Pred. No. 2.7e-232;
Matches 858; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3427 CATTAATGAATCGGCCCAACGCGCGGAGAGGCGGTTTGGTATTGGCGCTCTTCGCGCT 3486
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QY 3487 TCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCAC 3546
DB 68 TCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCAC 127

QY 3547 TCAAAGCGGTATACGGTTATCCACAGATCAGGGGATTAACGCGAGAAACATGTGA 3606
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DB 188 GCAAAAGCGCAGCAAAAGGCCAGCAACCGTAAAGGCCGCTGCTGGGCTTTTCCAT 247

QY 3667 AGGCTCGCCGCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGCGCAAC 3726
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QY 3787 GTTCGGACCTCGCGCTTACCGGATACGTGCGCCCTTCTCCCTTCGGAGCGGTGGCG 3846
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QY 3847 CTTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGGTGCTTGGCTCAAGCTG 3906
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QY 3907 GGCTGTGTGACGAAACCCCGCTTTCAGCCGACCGCTGCGCTTATCCGTPAATATCGT 3966
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QY 4087 GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGTAAGCCAGTTTACCTCGGA 4146
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QY 4207 GTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTTT 4266
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QY 4267 TCTACGCGGTCTGACGCTCAGAGAAGAC 4293
DB 848 TCTACGCGGTCTGACGCTCAGTGAAC 874

RESULT 12
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DEFINITION Fragilariopsis cylindrus SMART cDNA library (Clontech)
Frangilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.
ACCESSION  CF269652
VERSION     CF269652.1 GI:33631539
KEYWORDS    EST.
SOURCE      Fragilariopsis cylindrus
ORGANISM    Fragilariopsis cylindrus
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Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.
1 (bases 1 to 1073)
Mock,T. and Valentin,K.
EST analysis of freezing tolerance in the Antarctic diatom
Fragilariopsis cylindrus: Detection of numerous cold adaption
related genes and gene transfer events
Unpublished (2003)
Contact: Mock T
Biological Oceanography
Alfred-Wegener-Institute for Polar and Marine Research
Am Handelshafen 12, D-27570 Bremerhaven, Germany
Tel: +49 471 4831 1893
Fax: +49 471 4831 1425
Email: tmock@awi-bremerhaven.de
sequence with unknown function
PCR Primers
FORWARD: 5'lambdaTriplex2
BACKWARD: 3'lambdaTriplex2
Seq primer: ctgggaagcgcccatgtgtggt.
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/clone_lib="Antarctic"
/clone_lib="Fragilariopsis cylindrus SMART cDNA library
(Clontech)"
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first-strand synthesis with SMART IV oligos and CDS
III/3'PCR primer. Double strand cDNA synthesis was done by
LD PCR using the following program: 95oc for 5 min
denaturation and subsequent 20 cycles at 95oc (2min) and
68oc (6min). After SfiI digestion the cDNA was
fractionated with CHROMA Spin-400 columns. These cDNAs
were ligated overnight into pTriplex2 vectors."

ORIGIN
Query Match          15.4%; Score 835.6; DB 6; Length 1073;
Best Local Similarity 96.6%; Pred. No. 2.2e-227;
Matches 894; Conservative 0; Mismatches 24; Indels 7; Gaps 4;

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DB 1 GCTTCTGTCTCATGCGCGCTTTCCAGTCCGGAAACCTGTGTCGCCAGCTGCAATATGA 60

QY 3436 ATCGGCCAACCGCGCGGAGAGCGGTTTCGTTATTCGGCGCTTCCGCTTCCGCTC 3495
DB 61 ATCGGCCAACCGCGCGGAGAGCGGTTTCGTTATTCGGCGCTTCCGCTTCCGCTC 120

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Db 616 GTGGCGAAACCCGACAGGACTATAAGATACGAGGCGTTTCCCGCTGGAGACTCCCTCGT 675
QY 3777 GCGCTCTCCGTTCGACCGCTGCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGG 3836
Db 676 GCGCTCTCCGTTCGACCGCTGCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGG 735
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Db 736 AAGCGTGGCGCTTCTCATAGCTCACGCTGAGGTATCTCAGTTCCGCTGAGTTCGTTG 795
QY 3897 CTCGAAGCTGGGCTGTGTGACAGAACCCCGGTTACGCGGACGCGTGGCGCTTATCCGG 3956
Db 796 CTCGAAGCTGGGCTGTGTGACAGAACCCCGTTCGTTACGCGGACGCGCTTATCCGG 855
QY 3957 TAACTATCGTCTTGAGTCCAAACCGGTAAGACACGACTTATGCGCACTGGCAGCAGCAC 4016
Db 856 TAACTATCGTCTTGAGTCCAAACCGGTAAGACACGACTTATGCGCGCTGACGACCCAC 915
QY 4017 TGSTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTG 4076
Db 916 TGSTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTG 974
QY 4077 GCCTAATACGGCTACACTAGAGAAACAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGT 4136
Db 975 GCCCAACTACGGCTACCTAAAAAACACTATTTGGAAATCGCGCCCTCGCGAAACCCCTT 1034
QY 4137 TACCTTCGGAAAGAGTGTGTAGCTCTTGATCGGCAACACACGCTGTGTAGCGG 4196
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RESULT 14
LOCUS CL021193
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genomic survey sequence.
ACCESSION CL021193
VERSION CL021193.1 GI:40463006
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 1025)
Kremiczki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACCACTCACTATAGGAGA
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/sex="male"
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BAC library"

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Query Match 15.2%; Score 823.2; DB 10; Length 1025;
Best Local Similarity 95.7%; Pred. No. 7.8e-224;
Matches 900; Conservative 0; Mismatches 33; Indels 7; Gaps 5;

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QY 3355 GTGAGCTTAATCAATTAATTGGCTTCGCTCACTGCC--GCTTTCCAGTCGGGAAACC 3412
Db 207 GTGACCTAATCAATTAATTGGCTTCGCTCACTGCCAGACTTTCCAATCGGAAACC 266
QY 3413 TGTGCTGCAGCTGCATTAATGAATCGGCCAAGCGCGGG--GAGAGCGGTTTGCCTAT 3470
Db 267 TGTGCTGCCAGCTGCATTAATGAATCGGCCAAGCGCGGGAGAGACGCGTTTGCCTAT 326
QY 3471 TGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCGCG 3530
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Db 387 AGCGGTATCAGCTCACTCAAAAGCGGTAAATACAGTTATCCACAAAATCATGGGATAACGC 446
QY 3591 AGGAAAGAACATGTGAGCAAAAAGCGCGAAGAAAGCGCAGGAAACCGTAAAAAGCGCGTT 3650
Db 447 AGGAAAGAACATGTGAGCAAAAAGCGCAGCAAAAAGCGCAGGAAACCGTAAAAAGCGCGTT 506
QY 3651 GCTGGGCTTTTCCATAGGCTCGCCCCCTGACGAGCATCACAAAATCAGCCTCAAG 3710
Db 507 ACTGGCGTTTTTCCATAAGCTCCGCCCCCTGACGAGCATCACAAAATCAGCCTCAAG 566
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QY 3951 ATCCGCTAACTATCTGTTTGAAGTCCAAACCCGGTAAAGACAGACTTATCGCACTGGCAGC 4010
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RESULT 15
AU081044 1163 bp mRNA linear EST 30-JUL-2002
LOCUS AU081044 Oncorhynchus mykiss Kidney infected by infectious
DEFINITION hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KBI,
mRNA sequence.
ACCESSION AU081044
VERSION AU081044.1 GI:6431392
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 1163)
Kono,T., Sakai,M. and LaPatra,S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.

FEATURES
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/clone="KB1"
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infectious hematopoietic necrosis virus"
/notes="common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"

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Best Local Similarity 99.8%; Pred. No. 5.2e-223;
Matches 832; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 3267 GTTTCCTGTGTGAAATTTATCCGCTCACAATTTCCACACATACGAGCCGGGAAGCAT 3326
Db 391 GTTTCCTGTGTGAAATTTATCCGCTCACAATTTCCACACATACGAGCCGGGAAGCAT 450
QY 3327 AAAGTGTAAAGCTGGGGTGCCTAAATGAGTGAGCTAACTACATTAATTCGGTTGGGCTC 3386
Db 451 AAAGTGTAAAGCTGGGGTGCCTAAATGAGTGAGCTAACTACATTAATTCGGTTGGGCTC 510
QY 3387 ACTGCCCGCTTTCAGTTCGGGAACCTGTCGTCGAGCTGCATTAAATGAATCGGCCAACG 3446
Db 511 ACTGCCCGCTTTCAGTTCGGGAACCTGTCGTCGAGCTGCATTAAATGAATCGGCCAACG 570
QY 3447 CGCGGGGAGAGGGGTTTGGTATTTGGGCGCTCTTCGCTTTCCTCGCTCACTGACTCGCT 3506
Db 571 CGCGGGGAGAGGGGTTTGGTATTTGGGCGCTCTTCGCTTTCCTCGCTCACTGACTCGCT 630
QY 3507 GCGCTCGGTCGTTGCGGCTGCGGAGCGGTTATCAGCTCACTCAAAGCGGTAATACGGTT 3566
Db 631 GCGCTCGGTCGTTGCGGCTGCGGAGCGGTTATCAGCTCACTCAAAGCGGTAATACGGTT 690
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Search completed: February 21, 2006, 00:22:34
Job time : 19475 secs

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; MOLECULE TYPE: cDNA									
us-08-472-809B-8									
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Best Local Similarity 99.2%; Pred. No. 0;									
Matches 5007; Conservative 0; Mismatches 4; Indels 37; Gaps 1;									
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Qy	473	TGAAGGTGAAGATGCAACCATGTCTCTCTCGATCTCTTCACTGTGGCGTGTGCTGTC	532						
Db	707	TGAAGGTGAAGATGCAACCATGTCTCTCTCGATCTCTTCACTGTGGCGTGTGCTGTC	766						
Qy	533	TCACCTTCACAGCTCTGCCAGGCTGGACCGGAGACGCTCTGCCGGGCTCAGCTGGTGG	592						
Db	767	TCACCTTCACAGCTCTGCCAGGCTGGACCGGAGACGCTCTGCCGGGCTCAGCTGGTGG	826						
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Db	827	ATGCTCTTTCAGTTTCGTGTGGAGACAGGGGCTTTTATTTCAACAAAGCCACAGGATG	886						
Qy	653	GCTCCAGAGCTGGAGGGGCGCTCAGACAGGTATCGTGTAGTGTGCTTCCGAGCT	712						
Db	887	GCTCCAGAGCTGGAGGGGCGCTCAGACAGGATCGTGTAGTGTGCTTCCGAGCT	946						
Qy	713	GTGATCTAAGGAGGCTGGAGATGATTGGCACCCCTCAAGCTGCCAAGTCAGCTCGCT	772						
Db	947	GTGATCTAAGGAGGCTGGAGATGATTGGCACCCCTCAAGCTGCCAAGTCAGCTCGCT	1006						
Qy	773	CTGTCCGTGCCAGCGCCACACCGACATGCCAAGACCCAGAGGAAATGATTTGAAGA	832						
Db	1007	CTGTCCGTGCCAGCGCCACACCGACATGCCAAGACCCAGAGGAAATGATTTGAAGA	1066						
Qy	833	ACGCAAGTAGAGGAGTGACAGGAAACAGAACTACAGGATGAGAAACCCCTCTGAGG	892						
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Db	1487	CAGTTGTTTCTGTATCATATTTTCCCTGGGCTTTTCCATCTCTCGCTGACCTGGGACTGGGT	1546						
Qy	1313	GCTGGGCTGGGAGCAGGGGTTGGGCTCTCCAGGGAGAGATGGCATGGGAGAGTGTATG	1372						
Db	1547	GCTGGGCTGGGAGCAGGGGTTGGGCTCTCCAGGGAGAGATGGCATGGGAGAGTGTATG	1606						
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2987	TTGCAGAAAGATTTTGGGAACAGATGAATGGAATTTCCACCAACAGAAAAATTTAAC	3046
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3227	GGGCTTTCCCTCTCTTCCATCGACGGGCTCACTATCAGCCCTGAAAGTCCAACCTTTCTGAA	3286
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DB 5567 CAGTGGCGAAAGGGGATGCTGCGAAGGGATTAAGTTGGGTAAAGCCAGGTTTTC 5626
QY 5356 CAGTCACGAGTGTGTAAGACGAGCGGCGAGTGAATGTAATACGACTCACTATAGGCGAA 5415
DB 5627 CAGTCACGAGTGTGTAAGACGAGCGGCGAGTGAATGTAATACGACTCACTATAGGCGAA 5686
QY 5416 TTGGAGCT 5423
DB 5687 TTGGAGCT 5694
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RESULT 2

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US-08-472-809B-7
; Sequence 7, Application US/08472809B
; Patent No. 5925564
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: DeMayo, Franco J.
; APPLICANT: O'Malley, Bert W.
; TITLE OF INVENTION: Expression Vector Systems and
; TITLE OF INVENTION: Method of Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
```

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; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,809B
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,846
; FILING DATE: March 9, 1994
; APPLICATION NUMBER: 07/789,919
; FILING DATE: No. 5925564ember 6, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 214/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6345 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-472-809B-7
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Query Match 51.4%; Score 2785.8; DB 2; Length 6345;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2787; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 413 CCATGGGAAAAATCAGCAGTCTTCCAAACCAATATTTAAAGTGTCTTTTGTGATTTCT 472
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QY 473 TGAAGGTGAAGATGCACACCATGTCTCTCGCATCTCTTCTACTCGCGCTGTGCTGCG 532
DB 3616 TGAAGGTGAAGATGCACACCATGTCTCTCTCGCATCTCTTCTACTCGCGCTGTGCTGCG 3675
QY 533 TCACCTTTCACACAGCTCTGCGCACCGGCTGCGACCGGAGACGCTCTGCGGGCTGAGCTGG 592
DB 3676 TCACCTTTCACACAGCTCTGCGCACCGGCTGCGACCGGAGACGCTCTGCGGGCTGAGCTGG 3735
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DB 3976 ACCCAAGTACAGGGAGTGCAGGAAACAAAGACTACAGATCTAGAGACCTCTCTGAGG 4035
QY 893 AGTGAAGAGTGACATGCCACCGCAGGATCCCGCGGCTGCGAGGAATTCGATGGGCCATCC 952
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Db 4156 GATGACAAATCTTGAGTTCCAGGCTGCTGAGGACCTCCACGAGCCATGCACTTTCTAT 4215
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Qy 1193 AAGGAAACATAAACTTCAAGAAGCAATAAATCATCAGTCATTTCTGTACACCCCTAATG 1252
Db 4336 AAGGAAACATAAACTTCAAGAAGCAATAAATCATCAGTCATTTCTGTACACCCCTAATG 4395
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Db 4516 GGNATCTGCTGGGGGGGGGAGTCAACCTGCTGTGGGCTGCAAGGAGCCCATTTGGTGCA 4575
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Db 4636 AGTAGGAAAGGGTTACGAGCGCGGTTCAATTTCTCAGCTTGTGAAGGATTTGTTGGGCTC 4695
Qy 1553 AGCTGCCAGAGCAGTAGCAGGATGCTGTGCGAGCTCCGAGCTGTGATGAGCAGAGGC 1612
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Db 4756 AAGGCTGCAAGCTGAGGCGCAGGTTGGGCGACAGGTTAAATTAAGAGCTTCCACTCCACT 4815
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Db 4816 TATGGAAGCCCTCTCGCACTCAACCTGTCCCTGGGCTGGGGGCGAGCCAGGGCCACTTC 4875
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Db 4936 CTCCTATAGTTGCTGTCGCTTAGGAGACCAAGGGGCTTCCCTGCTGGGCTTCTGGC 4995
Qy 1853 CCGGCGACACTCAGGAGCTGCCCTATCTGCTCTCTCTAGATGGTCTTGGCAGGAAGG 1912
Db 4996 CCGGCGACACTCAGGAGCTGCCCTATCTGCTCTCTCTAGATGGTCTTGGCAGGAAGG 5055
Qy 1913 CTGCACTTGCTGGGCTGATCCATATTAACCTCAGTAGGAGCAGCAGCTGCTGGAAG 1972
Db 5056 CTGCACTTGCTGGGCTGATCCATATTAACCTCAGTAGGAGCAGCAGCTGCTGGAAG 5115
Qy 1973 AAAAGATGATTTCAACTGACTTACTATCCAGGAGGTTATGCTTTTATTTGATGGTG 2032
Db 5116 AAAAGATGATTTCAACTGACTTACTATCCAGGAGGTTATGCTTTTATTTGATGGTG 5175

Qy 2033 CTAAGAGTGGTTCCTTCTCACTGTAAATGATTTTGCCCTCATGTGTGAATACACTTTCCA 2092
Db 5176 CTAAGAGTGGTTCCTTCTCACTGTAAATGATTTTGCCCTCATGTGTGAATACACTTTCCA 5235
Qy 2093 ATAAAGCAGCAGCTCCAAAGGAAATTTCTGAGGAGAGACAGTACCTGGTGGGAAG 2152
Db 5236 ATAAAGCAGCAGCTCCAAAGGAAATTTCTGAGGAGAGACAGTACCTGGTGGGAAG 5295
Qy 2153 TCCTGTGAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGAGCAGAT 2212
Db 5296 TCCTGTGAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGAGCAGAT 5355
Qy 2213 CACATCCTTTCTTAAAGAACAAACAGAAAGGTAGTGTGACCTTGTCTGTATTACTATT 2272
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Qy 2273 TAGCGCTTGTGTTAGTGGCAGATACCTCAACGGGGATATGGAGAGCTATTTCCCAAC 2332
Db 5416 TAGCGCTTGTGTTAGTGGCAGATACCTCAACGGGGATATGGAGAGCTATTTCCCAAC 5475
Qy 2333 CTTGCTGTGAGCCCTGATCTGGGCTTTTCTGTAGCTTAAAGCGGTGCCAAGTCTTAA 2392
Db 5476 CTTGCTGTGAGCCCTGATCTGGGCTTTTCTGTAGCTTAAAGCGGTGCCAAGTCTTAA 5535
Qy 2393 GTGATTTAGAAATCAGTAAGGCTGGAAAGAACACACAGATCATTTAAGTCCAAGTGTAGCC 2452
Db 5536 GTGATTTAGAAATCAGTAAGGCTGGAAAGAACACACAGATCATTTAAGTCCAAGTGTAGCC 5595
Qy 2453 CCATCCCCACGGGCCCATCTGTCACTCAGTGCCACATCCACGATTTCTTTGAACATCTCC 2512
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Qy 2513 AGGAGCAGTGACTCCACCCGTCCAGAGCTGTGCTTCCAGAGCAGGAGGAGTGTCTCA 2572
Db 5656 AGGAGCAGTGACTCCACCCGTCCAGAGCTGTGCTTCCAGAGCAGGAGGAGTGTCTCA 5715
Qy 2573 GTGCCAGTTGCTTCTGCTGAAGAGCTTAAACAGTGCAAGTTTAAACAGGAGCTGATTTGTT 2632
Db 5716 GTGCCAGTTGCTTCTGCTGAAGAGCTTAAACAGTGCAAGTTTAAACAGGAGCTGATTTGTT 5775
Qy 2633 GATGTGGTGTGGAATCAGTACGTTGAGATGTCTAAACCTTTTGGAGATTAATTTTCA 2692
Db 5776 GATGTGGTGTGGAATCAGTACGTTGAGATGTCTAAACCTTTTGGAGATTAATTTTCA 5835
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Qy 2753 TTGCGAGAAAGATTTGTTGGGAAACAGATGAATGGAAATTTCCACCAACAGAAATTTAAC 2812
Db 5896 TTGCGAGAAAGATTTGTTGGGAAACAGATGAATGGAAATTTCCACCAACAGAAATTTAAC 5955
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Db 5956 ACTTACACAGTTTGTGCTGCTGCTTGTGATGATTTCTTAAAGATCTCATCATCTCTCC 6015
Qy 2873 CTGCTCTTGAGCCAGGCTGCTGACAGGAGTGGAGGATCATCAGGCTCAGCATCTCTCAG 2932
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Qy 2933 CATCTAGGATGTGCACTATGTGTGATGGTGACACTTTTAGAGAACTGCTTTGATTTCCCA 2992
Db 6076 CATCTAGGATGTGCACTATGTGTGATGGTGACACTTTTAGAGAACTGCTTTGATTTCCCA 6135
Qy 2993 GGGCTTTTCCCTCTCTTCCATGAGGCTCATCTATCAGCCCTGAAAAGTCCAACTTTCTGAA 3052
Db 6136 GGGCTTTTCCCTCTCTTCCATGAGGCTCATCTATCAGCCCTGAAAAGTCCAACTTTCTGAA 6195
Qy 3053 CTTCCAGCAGCTGCTCTCTGAGGCTGTTCCATAGAGGCGCACAGGAGCTGTAGCCAG 3112
Db 6196 CTTCCAGCAGCTGCTCTCTGAGGCTGTTCCATAGAGGCGCACAGGAGCTGTAGCCAG 6255

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3113 GCATGACCTTTTCCAGCCGCTCTCTGAATCCAGCACTGTGCTGGAGGCAGCTCTGG
6256 GCATGACCTTTTCCAGCCGCTCTCTGAATCCAGCACTGTGCTGGAGGCAGCTCTGG
3173 TCCTGGGGTCTGCAGTGAGCCAGGGAACA 3202
6316 TCCTGGGGTCTGCAGTGAGCCAGGGAACA 6345

RESULT 3
US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synthesized
US-09-186-002-16

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3781	Qy	TCTCCTGTTCCGACCTGCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGC	384
6449	Db	TCTCCTGTTCCGACCTGCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGC	6508
3841	Qy	GTGGCGCTTCTCATAGCTCACGCTGTAGTATCTCAGTTTCGGTGTAGGTCTCGCTCC	3900
6509	Db	GTGGCGCTTCTCATAGCTCACGCTGTAGTATCTCAGTTTCGGTGTAGGTCTCGCTCC	6568
3901	Qy	AAGCTGGGCTGTGTGACGAACCCCGGTTACGCCGACCGCTGCGGCTTATCCGGTAAC	3960
6569	Db	AAGCTGGGCTGTGTGACGAACCCCGGTTACGCCGACCGCTGCGGCTTATCCGGTAAC	6628
3961	Qy	TATCGTCTTGAGTCCAAACCCCGGTAAACACGACTTATCGCCACTGCGCAGCAGCACTGGT	4020
6629	Db	TATCGTCTTGAGTCCAAACCCCGGTAAACACGACTTATCGCCACTGCGCAGCAGCACTGGT	6688
4021	Qy	AACAGATTAGCAGACGAGGTATGTAGGCGGTGTACAGAGTTCCTTGAAGTGGTGGCCT	4080
6689	Db	AACAGATTAGCAGACGAGGTATGTAGGCGGTGTACAGAGTTCCTTGAAGTGGTGGCCT	6748
4081	Qy	AACCTAGCGGTACACTAGAAGAAACAGTATTTGGTATCTGCGCTCTGCTGGAAGCCAGTTACC	4140
6749	Db	AACCTAGCGGTACACTAGAAGAAACAGTATTTGGTATCTGCGCTCTGCTGGAAGCCAGTTACC	6808
4141	Qy	TTCCGAAAAAGAGTGGTAGCTCTTGATCCGGCAAAACACACCGCTGCTAGCGGTGGT	4200
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4281	Qy	-----	4280
7109	Db	AACCTTTCATAGAAGGGCGGTGGATCGAAATCTCGTGATGCGAGTTGGGCGTCGCT	7168
4281	Qy	-----	4280
7169	Db	TGGTCGGTCACTTTCAACCCCGAGAGTCCCGCTCAGAAGAACTCGTCAAGAAAGCGCATAGA	7228
4313	Qy	AGGGATGCCCTGGGATCCGGAGCGCGATACGTTAAGCAAGAGAAAGCGGTTCAGCCCC	4372
7229	Db	AGGGATGCCCTGGGATCCGGAGCGCGATACGTTAAGCAAGAGAAAGCGGTTCAGCCCC	7288
4373	Qy	ATTCCGCGCCAAAGCTCTTTCAGCAATATCAAGGGTAGCCAAAGCTATGCTCTGATAGCGGT	4432
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4493	Qy	TATTCCGCAAGCAGGCATCCGCCATGGGTACAGACGATCCTCGCGCTCGGGCATGCGCG	4552
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4553	Qy	CCTTGAGCTGGCGAAACAGTTTCGGCTGGCGCGAGCCCTGATGCTCTTTCGTCAGATCAT	4612
7469	Db	CCTTGAGCTGGCGAAACAGTTTCGGCTGGCGCGAGCCCTGATGCTCTTTCGTCAGATCAT	7528
4613	Qy	CCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATCGGATGTTTCGCTT	4672


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Db 5416 GCTGCGAATCGGAGCGCGGCGATACCGTAAGACGAGGAGCGGTACGCCCATTCGCGCG 5357
Qy 4382 CAAGCTCTTCAGCAATATACGGGTAGCCAAACGCTATGCTCTGATAGCGGTTCGCCACAC 4441
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Qy 4802 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCAGAGTCGCGCAAGGAAACGCCG 4861
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Qy 5162 TTACTTTGCGGGCTTCCCACTTACCAGAGGCGCCCGAGCTGGCAATTCGCGTTTCG 5221
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Db 4456 GCCTTCTCTT 4447
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RESULT 5

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US-09-554-572-3/c
; Sequence 3, Application US/09554572
; Patent No. 6573091
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY, INC.
; TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 228,000,302,01
; CURRENT APPLICATION NUMBER: US/09/554,572
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 8574
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector
; OTHER INFORMATION: construct for pVLMB3
US-09-554-572-3
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Query Match 27.1%; Score 1470; DB 3; Length 8574;
Best Local Similarity 91.7%; Pred. No. 6.7e-314;
Matches 1604; Conservative 0; Mismatches 80; Indels 66; Gaps 2;

Qy 3608 CAAAAGGCCAGCAAAAGGCCAGCAACCGTAAAAAGGCCGGTTGCTGGCGTTTTTCCATA 3667
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Qy 3668 GGCTCCGCCCCCTCGAGCAGCATCAAAAATCAGCCTCAAGTCAGAGTGGCGAAACC 3727
Db 7915 GGCTCCGCCCCCTCGAGCAGCATCAAAAATCAGCCTCAAGTCAGAGTGGCGAAACC 7856
Qy 3728 CGACAGACTATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTGGTGGCTCTCTG 3787
Db 7855 CGACAGACTATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTGGTGGCTCTCTG 7796
Qy 3788 TTCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCG 3847
Db 7795 TTCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCG 7736
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Qy 4262 T----- 4262
Db 7315 TAGAAGCGCGGTGGAAATCGAAATCTCGTGTAGCGAGTTGGCGTCTGCTTGGTGGTC 7256
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4263 -CTTTTCTACGGGCTGACGCTCAGAAAGAACTCGTCAAGAGCGCGATAGAGCGGATGC 4321
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 4562 TGGCGAACAGTTCGGCTGGCGCGAGCCCTGATGCTCTTCTCGTCCAGATCATCTCTGATCGA 4621
 6955 TGGCGAACAGTTCGGCTGGCGCGAGCCCTGATGCTCTTCTCGTCCAGATCATCTCTGATCGA 6896
 4622 CAAGACCGGCTTCATCCGAGTACGCTGCTCGCTCGATGCGATGTTTGGTGGTTCGA 4681
 6895 CAAGACCGGCTTCATCCGAGTACGCTGCTCGCTCGATGCGATGTTTGGTGGTTCGA 6836
 4682 ATGGGAGGTAGCGGATCAAGCGTATGACGCGCGCGCATGTCATGATGATGATGATGAT 4741
 6835 ATGGGAGGTAGCGGATCAAGCGTATGACGCGCGCGCATGTCATGATGATGATGATGATGAT 6776
 4742 CTCTTCGCGAGGAGCAAGGTAGATGACAGGAGATCTCTCGCGCGCATCTTCGCCCAATA 4801
 6775 CTCTTCGCGAGGAGCAAGGTAGATGACAGGAGATCTCTCGCGCGCATCTTCGCCCAATA 6716
 4802 GCAGCGAGTCCCTTCGCTTTCAGTGAACAAGTGCAGACAGTGTGGCAAGAACGCCCG 4861
 6715 GCAGCGAGTCCCTTCGCTTTCAGTGAACAAGTGCAGACAGTGTGGCAAGAACGCCCG 6656
 4862 TCCTGGCGACGACGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4921
 6655 TCCTGGCGACGACGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6596
 4922 GGTGCGTCTTGAACAAAGAACCGGCGCCCTGCGCTGACAGCGGAAACACGCGCGCAT 4981
 6595 GGTGCGTCTTGAACAAAGAACCGGCGCCCTGCGCTGACAGCGGAAACACGCGCGCAT 6536
 4982 CAGAGCGCGATGCTGTGTGTCGCGCAGTCATAGCGGAATAGCTCTCCACCAAGCGG 5041
 6535 CAGAGCGCGATGCTGTGTGTCGCGCAGTCATAGCGGAATAGCTCTCCACCAAGCGG 6476
 5042 CCGGAGAACCTGCGTCAATCCATCTGTTCAATCATGCGGAACGATCCTCATCTGCTCT 5101
 6475 CCGGAGAACCTGCGTCAATCCATCTGTTCAATCATGCGGAACGATCCTCATCTGCTCT 6416
 5102 CTTGATCAGATCTTGATCCCTGCGCATCAGATCTCTTGGCGCAAGAAAGCCATCCAGT 5161
 6415 CTTGATCAGATCTTGATCCCTGCGCATCAGATCTCTTGGCGCAAGAAAGCCATCCAGT 6356
 5162 TTACTTTGCGGGGTTCCCAACCTTACAGAGGCGCGCCAGCTGGCAATTCGGTTCGC 5221
 6355 TTACTTTGCGGGGTTCCCAACCTTACAGAGGCGCGCCAGCTGGCAATTCGGTTCGC 6296
 5222 TTGCTGTCCATAAACCGCGCAGTCTAGCACTGTTGGGAAGGGCGATCGGTGGGGCCT 5281
 6295 TTGCTGTCCATAAACCGCGCAGTCTAGCACTGTTGGGAAGGGCGATCGGTGGGGCCT 5281
 5282 CTTGCTGCTATT 5291
 6235 GCTTTCTCTT 6226

RESULT 6
 US-09-380-190A-23/c
 ; Sequence 23, Application US/09380190A
 ; Patent No. 6410220
 ; GENERAL INFORMATION:
 ; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
 ; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
 ; THEREOF
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
 ; STREET: 119 NORTH FOURTH STREET, SUITE 203
 ; CITY: MINNEAPOLIS
 ; STATE: MINNESOTA
 ; COUNTRY: USA
 ; ZIP: 55401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/380,190A
 ; FILING DATE: 26-Aug-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US98/03918
 ; FILING DATE: 28-FEB-98
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MUEITING, ANN M.
 ; REGISTRATION NUMBER: 33,977
 ; REFERENCE/DOCKET NUMBER: 228.00010201
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-305-1217
 ; TELEFAX: 612-305-1228
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9093 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-380-190A-23
 Query Match 27.1%; Score 1470; DB 3; Length 9093;
 Best Local Similarity 91.7%; Pred.No. 6.7e-314;
 Matches 1604; Conservative 0; Mismatches 80; Indels 66; Gaps 2;
 QY 3608 CAAAAGCGCCAGCAAAAGCGCCAGGAACCGTAAAGAGCGCGTTCCTGCGGCTTTTCCATA 3667
 DB 8494 CAATAATAGCGCCAGGTTCTCGAGGCGGCATCTCGGCGTTCCTGCGGCTTTTCCATA 8435
 QY 3668 GGCTCGCGCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGGAAACC 3727
 DB 8434 GGCTCGCGCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGGAAACC 8375
 QY 3728 CGACAGACTATAAAGATACAGGCGGTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTG 3787
 DB 8374 CGACAGACTATAAAGATACAGGCGGTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTG 8315
 QY 3788 TTCGAGCCCTGCGGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGGAAGCGTGGCGC 3847
 DB 8314 TTCGAGCCCTGCGGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGGAAGCGTGGCGC 8255
 QY 3848 TTTCTCATAGCTCACGCTGTAGTATCTCAGTTTCGCTGTAGTGTGCTTCCGCTCAAGCTGG 3907
 DB 8254 TTTCTCAATGCTCACGCTGTAGTATCTCAGTTTCGCTGTAGTGTGCTTCCGCTCAAGCTGG 8195
 QY 3908 GCTGTGTGACGAAACCCCGGTTACGCGCGCTTCAGCGCGCTTATCCGGTAACTATCGTC 3967
 DB 8194 GCTGTGTGACGAAACCCCGGTTACGCGCGCTTATCCGGTAACTATCGTC 8135

Qy 3968 TTGAGTCCAAACCCGGTAAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAAACAGGA 4027
Db 8134 TTGAGTCCAAACCCGGTAAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAAACAGGA 8075
Qy 4028 TTAGCAGAGCAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCCTAACTACG 4087
Db 8074 TTAGCAGAGCAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCCTAACTACG 8015
Qy 4088 GCTACACTAGAAAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTTCGGAA 4147
Db 8014 GCTACACTAGAAAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTTCGGAA 7955
Qy 4148 AAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACCCAGCTGTGTAGCGGTGTTTTTTG 4207
Db 7954 AAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACCCAGCTGTGTAGCGGTGTTTTTTG 7895
Qy 4208 TTTCGAAGCAGCAGATACG-----CGCAGAAAAAAGAGTCTCAAGAGAGATCCTTTGA 4261
Db 7894 TTTCGAAGCAGCAGATACGAAATCCGTCGCGGAACAGATTCCGAAGCCCAACCTTTCA 7835
Qy 4262 T----- 4262
Db 7834 TAGAAGCGCGGTGGGAATCGAAATCTCGTGAAGCGAGGTTGGCGTGGCTTCGGTC 7775
Qy 4263 -CTTTTCTACGGGGTCTGACGCTCAGAAAGACTCGTCAAGAAAGCGGATAGAAAGCGCATGC 4321
Db 7774 ATTTGGAACCCAGATCCCGCTCAGAAAGACTCGTCAAGAAAGCGGATAGAAAGCGCATGC 7715
Qy 4322 GCTCGAATCGGAGCGCGGATACCGTAAAGCAGAGAAAGCGGTGACGCCATTCGCGCG 4381
Db 7714 GCTCGAATCGGAGCGCGGATACCGTAAAGCAGAGAAAGCGGTGACGCCATTCGCGCG 7655
Qy 4382 CAAGCTCTTACGCAATATCAGGCTAGCCAGCTATGTCTGTATAGGGTTCGCCACAC 4441
Db 7654 CAAGCTCTTACGCAATATCAGGCTAGCCAGCTATGTCTGTATAGGGTTCGCCACAC 7595
Qy 4442 CCAGCGGCCACAGTCTGATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCA 4501
Db 7594 CCAGCGGCCACAGTCTGATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCA 7535
Qy 4502 AGCAGGCATCCCATGGGTACAGACGAGATCCTCGCGTGGGATGCGGCCCTTGAGCC 4561
Db 7534 AGCAGGCATCCCATGGGTACAGACGAGATCCTCGCGTGGGATGCGGCCCTTGAGCC 7475
Qy 4562 TGGCGACAGTTCCGCTGGCGGAGCCCTGATCTTGTGTCAGATCATCTCTGATCGA 4621
Db 7474 TGGCGACAGTTCCGCTGGCGGAGCCCTGATCTTGTGTCAGATCATCTCTGATCGA 7415
Qy 4622 CAAGACCGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGA 4681
Db 7414 CAAGACCGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGA 7355
Qy 4682 ATGGCAGGTAGCCCGATCAAGCGTATGACGCGCCGATTCGATCGACCCATGATGATA 4741
Db 7354 ATGGCAGGTAGCCCGATCAAGCGTATGACGCGCCGATTCGATCGACCCATGATGATA 7295
Qy 4742 CTTTCTCGCAGGACAGGTGAGATGACAGAGATCTCTGCCCCGACACTTCGCCCAATA 4801
Db 7294 CTTTCTCGCAGGACAGGTGAGATGACAGAGATCTCTGCCCCGACACTTCGCCCAATA 7235
Qy 4802 GCAGCAGTCCCTTCCCGCTTCAGTGAACAGTTCGAGCAGACAGTCTGCGCAAGAACGCGCG 4861
Db 7234 GCAGCAGTCCCTTCCCGCTTCAGTGAACAGTTCGAGCAGACAGTCTGCGCAAGAACGCGCG 7175
Qy 4862 TCGTGGCAGCCAGATAGCCCGCTGCTCGTCTGCAAGTTCAATTCAGGCAACGCGACA 4921
Db 7174 TCGTGGCAGCCAGATAGCCCGCTGCTCGTCTGCAAGTTCAATTCAGGCAACGCGACA 7115
Qy 4922 GGTGGCTTTGACAAAAAGAACCGGCGCCCTGCGCTGACAGCGGACACGCGGCAT 4981
Db 7114 GGTGGCTTTGACAAAAAGAACCGGCGCCCTGCGCTGACAGCGGACACGCGGCAT 7055
Qy 4982 CAGAGCAGCCGATGTCTGTTGTGCCAGTCAAGCCGATAGCCGATAGCCTTCCACCCCAAGCGG 5041

Db 7054 CAGAGCAGCCGATGTCTGTTGTGCCAGTCATAGCCGAATAGCTCTCCACCCAAAGCGG 6995
Qy 5042 CCGGAGAACCTCGTGAATCCATCTTGTTCATCATGCGAAACGATCTCTCATCTGTCT 5101
Db 6994 CCGGAGAACCTCGTGAATCCATCTTGTTCATCATGCGAAACGATCTCTCATCTGTCT 6935
Qy 5102 CTTGATCAGATCTTGATCCCTCGCGCATCAGATCTTGGCGCAAGAAAGCCATCCAGT 5161
Db 6934 CTTGATCAGATCTTGATCCCTCGCGCATCAGATCTTGGCGCAAGAAAGCCATCCAGT 6875
Qy 5162 TTACTTTGAGGGGTTCCCAACCTTACCAGAGGCGGCCAGCTGGCAATTCGGTTCCG 5221
Db 6874 TTACTTTGAGGGGTTCCCAACCTTACCAGAGGCGGCCAGCTGGCAATTCGGTTCCG 6815
Qy 5222 TTCTGTTCATAAAACCGCCAGCTAGCAACTGTTGGGAAGCGGCATCGGTGGGSCCT 5281
Db 6814 TTCTGTTCATAAAACCGCCAGCTAGCTATTCGCATGTAAGCCCACTGCAAGCTACCT 6755
Qy 5282 CTTTCGGCTATT 5291
Db 6754 GCTTCTCTT 6745

RESULT 7
US-09-554-572-2/c
; Sequence 2, Application US/09554572
; Patent No. 6573091
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY, INC.
; TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 228.00030201
; CURRENT APPLICATION NUMBER: US/09/554,572
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9093
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector
; OTHER INFORMATION: construct for pVLMB2
US-09-554-572-2

Query Match 27.1%; Score 1470; DB 3; Length 9093;
Best Local Similarity 91.7%; Pred. No. 6.7e-314;
Matches 1604; Conservative 0; Mismatches 80; Indels 66; Gaps 2;
Qy 3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGGTTCGTCGGCGTTTTCATATA 3667
Db 8494 CAATAATAGGCCAGGGTTCTCGAGGCGCGCATCTCGGGTGTGCTGGCGTTTTCATATA 8435
Qy 3668 GGCTCCCGCCCTTCGAGCAGCATCAAAAATCGAGCTCAAGTCAGAGGTGGCGAAACC 3727
Db 8434 GGCTCCCGCCCTTCGAGCAGCATCAAAAATCGAGCTCAAGTCAGAGGTGGCGAAACC 8375
Qy 3728 CGACAGACTATTAAGATACAGGCGTTTCCCTCGGAAGTCCCTCGTGGCTCTCTG 3787
Db 8374 CGACAGACTATTAAGATACAGGCGTTTCCCTCGGAAGTCCCTCGTGGCTCTCTG 8315
Qy 3788 TTCCGACCTCGCGTTTACCGGATACCTGTCCGCTTTCCTTCGGGAAGCGTGGCGC 3847
Db 8314 TTCCGACCTCGCGTTTACCGGATACCTGTTCGCGTTTCTCCCTTCGGGAAGCGTGGCGC 8255
Qy 3848 TTTCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGTTAGTGTAGTTCGTTCCAAAGCTGG 3907
Db 8254 TTTCTCAATGCTCAGCTGTAGGTATCTCAGTTTCGTTAGTGTAGTTCGTTCCAAAGCTGG 8195
Qy 3908 GCTGTGTGACGAAACCCCGCTTACGCGCCAGCCGCTGCGCTTATCCGGTAACTATCGTC 3967
Db 8194 GCTGTGTGACGAAACCCCGCTTACGCGCCAGCCGCTGCGCTTATCCGGTAACTATCGTC 8135

QY 3968 TTGAGTCCAAACCCGGTAAAGACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGA 4027
 Db 8134 TTGAGTCCAAACCCGGTAAAGACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGA 8075
 QY 4028 TTAGCAGAGCGAGGTATGTAGGCGGTCTACAGAGTCTTGAAGTGGTGGCCTAACTACG 4087
 Db 8074 TTAGCAGAGCGAGGTATGTAGGCGGTCTACAGAGTCTTGAAGTGGTGGCCTAACTACG 8015
 QY 4088 GCTACACTAGAAAGCAAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTATACCTTCGGAA 4147
 Db 8014 GCTACACTAGAAAGCAAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTATACCTTCGGAA 7955
 QY 4148 AAGAGTGTGTAGTCTTTGATTCGGGCAAAACAAACCCAGCTGTGTAGCGGTGGTTTTTTG 4207
 Db 7954 AAGAGTGTGTAGTCTTTGATTCGGGCAAAACAAACCCAGCTGTGTAGCGGTGGTTTTTTG 7895
 QY 4208 TTTGCAAGCAGCAGATTACG-----CGCAAAAGAAAGATCTCAAGAGATCTTTGA 4261
 Db 7894 TTTGCAAGCAGCAGATTACGATTTCGTCCTCGGAAACGATTCGGAAGCCCAACCTTTCA 7835
 QY 4262 T----- 4262
 Db 7834 TAGAAGCGCGGTGGAAATCTCGTATGGCAGGTTGGCGTGGCTTGGTCGGTC 7775
 QY 4263 -CTTTCTACGGGTCTGACGCTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAAGCGGATGC 4321
 Db 7774 ATTTGCAAAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAAGCGGATGC 7715
 QY 4322 GCTGCGAATCGGAGCGCGGATACCGTAAAGCAGGAGAGCGGTGAGCCCATTCGCGC 4381
 Db 7714 GCTGCGAATCGGAGCGCGGATACCGTAAAGCAGGAGAGCGGTGAGCCCATTCGCGC 7655
 QY 4382 CAAGCTCTTCAGCAATATACAGGCTAGCAAGCTATGCTCTGATAGCGTTCGCCACAC 4441
 Db 7654 CAAGCTCTTCAGCAATATACAGGCTAGCAAGCTATGCTCTGATAGCGTTCGCCACAC 7595
 QY 4442 CCAGCGCGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCA 4501
 Db 7594 CCAGCGCGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCA 7535
 QY 4502 AGCAGGATCCGATGGGTCAAGCGATCTCGCGCTGGGATGCGGCGCTTGAAGCC 4561
 Db 7534 AGCAGGATCCGATGGGTCAAGCGATCTCGCGCTGGGATGCGGCGCTTGAAGCC 7475
 QY 4562 TGGCAACAGTTCGGCTGGCGCGAGCCCTGATGCTCTTCTGATCAGATCATCTGATCGA 4621
 Db 7474 TGGCAACAGTTCGGCTGGCGCGAGCCCTGATGCTCTTCTGATCAGATCATCTGATCGA 7415
 QY 4622 CAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTGGCTTGGTGGTGA 4681
 Db 7414 CAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTGGCTTGGTGGTGA 7355
 QY 4682 ATGGGAGGTAGCGGATCAAGCGTATGAGCGCGCGCATTTGATCAGCATGATGATGA 4741
 Db 7354 ATGGGAGGTAGCGGATCAAGCGTATGAGCGCGCGCATTTGATCAGCATGATGATGA 7295
 QY 4742 CTTTCTCGGAGGAGTGTAGATGACAGAGATCTTCTGCTGATGATGATGATGATGATGAT 4801
 Db 7294 CTTTCTCGGAGGAGTGTAGATGACAGAGATCTTCTGCTGATGATGATGATGATGATGAT 7235
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 Db 7234 GCAGCCAGTCCCTTCCCGCTTTCAGTGAACAGTCTGAGCAGAGTTCGCGAGGAAAGCGCCG 7175
 QY 4862 TCGTGGCAGCAGATAGCGCGCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGAT 4921
 Db 7174 TCGTGGCAGCAGATAGCGCGCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGAT 7115
 QY 4922 GGTGGTCTTGAAGAAAGAACCGGCGCCCTGCTGCTGATGATGATGATGATGATGATGATGAT 4981
 Db 7114 GGTGGTCTTGAAGAAAGAACCGGCGCCCTGCTGCTGATGATGATGATGATGATGATGATGAT 7055

QY 4982 CAGAGCAGCGGATGTCTGTGTGCCAGTATAGCCGAATAGCCTCTCCACCAAGCGG 5041
 Db 7054 CAGAGCAGCGGATGTCTGTGTGCCAGTATAGCCGAATAGCCTCTCCACCAAGCGG 6995
 QY 5042 CCGGAAACCTCGTCCCAATCCATCTTGTTCATCATCGGAAACGATCCCTCATCCTGTCT 5101
 Db 6994 CCGGAAACCTCGTCCCAATCCATCTTGTTCATCATCGGAAACGATCCCTCATCCTGTCT 6935
 QY 5102 CTTGATCAGATCTTGTATCCCTCGGCCATCAGATCTTGGCGCAAGAAAGCCATCCAGT 5161
 Db 6934 CTTGATCAGATCTTGTATCCCTCGGCCATCAGATCTTGGCGCAAGAAAGCCATCCAGT 6875
 QY 5162 TTAATTTGAGGCGTTCACCACTTACAGAGGCGGCCAGCTGGCAATTCGCGTTCCG 5221
 Db 6874 TTAATTTGAGGCGTTCACCACTTACAGAGGCGGCCAGCTGGCAATTCGCGTTCCG 6815
 QY 5222 TTGCTCTCATAAACCGCCAGCTAGCAACTGTTGGGAAGGCGATCGGTGGGCGCT 5281
 Db 6814 TTGCTCTCATAAACCGCCAGCTAGCTATGCCATGTAAAGCCCACTGCAAGCTACCT 6755
 QY 5282 CTTTCGCTATT 5291
 Db 6754 GCTTCTCTT 6745
 RESULT 8
 US-09-554-572-1/c
 ; Sequence 1, Application US/09554572
 ; Patent No. 6573091
 ; GENERAL INFORMATION:
 ; APPLICANT: NATURE TECHNOLOGY, INC.
 ; TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
 ; TITLE OF INVENTION: SEQUENCES
 ; FILE REFERENCE: 228.00030201
 ; CURRENT APPLICATION NUMBER: US/09/554,572
 ; CURRENT FILING DATE: 2000-09-18
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 9145
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: vector
 ; OTHER INFORMATION: construct for pVLMB1
 US-09-554-572-1
 Query Match 27.1%; Score 1470; DB 3; Length 9145;
 Best Local Similarity 91.7%; Pred. No. 6.7e-314;
 Matches 1604; Conservative 0; Mismatches 80; Indels 66; Gaps 2;
 QY 3608 CAAAAGCCAGCAAAAGGCGCAGCAACCGTAAAGAGCGCGTGTGGCGTTTTCCTATA 3667
 Db 8546 CAATAATAGCGCCAGGGTTCCTGAGGCGGCGCATCTCGGCGTGTGGCGTTTTCCTATA 8487
 QY 3668 GGCTCGCGCCCTCGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCGAAACC 3727
 Db 8486 GGCTCGCGCCCTCGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCGAAACC 8427
 QY 3728 CGACGAGCTATAAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTG 3787
 Db 8426 CGACGAGCTATAAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTG 8367
 QY 3788 TTCCGACCTCGCGCTTACCGGATACCTGTCGCTTCTCCCTCGGGAAGCGTGGCG 3847
 Db 8366 TTCCGACCTCGCGCTTACCGGATACCTGTCGCTTCTCCCTCGGGAAGCGTGGCG 8307
 QY 3848 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTCTGTTCCGTCGAAGCTGG 3907
 Db 8306 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTCTGTTCCGTCGAAGCTGG 8247
 QY 3908 GCTGTGTGCAAGAACCCCGGTTACGCGCGGCTTATCGGCTTATCGGTAATATCGTC 3967

Matches 1600; Conservative 0; Mismatches 74; Indels 66; Gaps 2;

QY 3618 GCAAAAGCCAGGAACCGTAAAGGCGGCTTCTGCTGGCGTCTTTTCCATAGGCTCGCGCC 3677
DB |||||
QY 3273 GCAGGTGTACTCGAGGCGGCGATCTCGGCTTCTGCTGGCGTCTTTCCATAGGCTCGCGCC 3214
DB |||||
QY 3678 CCTGAGCAGCATCACAAAATCGAGCTCAAGTCAGAGTGCGGAAACCCGACAGACT 3737
DB |||||
QY 3213 CCTGACAGCATCACAAAATCGAGCTCAAGTCAGAGTGCGGAAACCCGACAGACT 3154
DB |||||
QY 3738 ATAAAGATACAGCGCTTCCCTCGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCT 3797
DB |||||
QY 3153 ATAAAGATACAGCGCTTCCCTCGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCT 3094
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QY 3798 GCCGCTTACCGGATACCTGCTCCGCTTTCTCCCTTCGGGAAGCTGGCGCTTTCTCATAG 3857
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QY 3093 GCCGCTTACCGGATACCTGCTCCGCTTTCTCCCTTCGGGAAGCTGGCGCTTTCTCAATG 3034
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QY 3858 CTACCGCTGATGATCTCAGTTCCGCTGATGCTGCTCCAGCTGGGCTGTGTGCA 3917
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QY 3033 CTACCGCTGATGATCTCAGTTCCGCTGATGCTGCTCCAGCTGGGCTGTGTGCA 2974
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QY 3918 CGAACCCCGCTTACGCGCCGACCGCTGCGCTTATCCGGTAACTATCGCTCTCAGTCCAA 3977
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QY 2973 CGAACCCCGCTTACGCGCCGACCGCTGCGCTTATCCGGTAACTATCGCTCTCAGTCCAA 2914
DB |||||
QY 3978 CCGGTAAGACAGGACTTATCGCCACTTGGCAGCAGCCACTTGGTAAACAGGATTAAGCAGC 4037
DB |||||
QY 2913 CCGGTAAGACAGGACTTATCGCCACTTGGCAGCAGCCACTTGGTAAACAGGATTAAGCAGC 2854
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QY 4038 GAGGTATGTAAGCGGTGCTACAGAGTTCTTGAAGTGCTGCCCTTAACTACGGCTACACTAG 4097
DB |||||
QY 2853 GAGGTATGTAAGCGGTGCTACAGAGTTCTTGAAGTGCTGCCCTTAACTACGGCTACACTAG 2794
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QY 4098 AAGACAGTATTTGGTATCTCGCTCTGCTGAGCGGAGTTACCTCGGAAAGAGTTGG 4157
DB |||||
QY 2793 AAGACAGTATTTGGTATCTCGCTCTGCTGAGCGGAGTTACCTCGGAAAGAGTTGG 2734
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QY 4158 TAGCTCTTGATCCGGCAAAACAAACCAACCGCTGCTGAGCGGTGTTTCTTGTTCGAAGCA 4217
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QY 2733 TAGCTCTTGATCCGGCAAAACAAACCAACCGCTGCTGAGCGGTGTTTCTTGTTCGAAGCA 2674
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QY 4218 GCAGATTACG-----CGCAGAAAAAAGGATCTCAAGAGATCTTTTGTAT----- 4262
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QY 2673 GCAGATTACGAAATTCGCTCCGGAAGAACGATTCGAAGCCCAACCTTCATAGAAGCGG 2614
DB |||||
QY 4263 -----CTTTTCTAC 4271
DB |||||
QY 2613 CGGTGGAATCGAAATCTGTGATGCGAGGTTGGCGTTCGCTTGGTCAATTCGAACC 2554
DB |||||
QY 4272 GGGGTCTGACGCTCAGAGAACTCGTCAAGAGCGGATAGAGCGGATGCGTCCGAATC 4331
DB |||||
QY 2553 CCAGGTCCGCTCAGAGAACTCGTCAAGAGCGGATAGAGCGGATGCGTCCGAATC 2494
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QY 4332 GGGAGCGGCGATACCGTAAAGCAGGAGAGCGGTGAGCCATTCGCGCCAAAGCTCTTC 4391
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QY 2493 GGGAGCGGCGATACCGTAAAGCAGGAGAGCGGTGAGCCATTCGCGCCAAAGCTCTTC 2434
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QY 4392 AGCAATATCACGGGTAGCCAAACGATATGCTGATAGCGGTGCGCACACCCAGCGCGCC 4451
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QY 2433 AGCAATATCACGGGTAGCCAAACGATATGCTGATAGCGGTGCGCACACCCAGCGCGCC 2374
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QY 4452 ACAGTCGATCAATCCAGAAAGCGGCAATTTCCACCATGATATTCGGCAAGCAGGCATC 4511
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QY 2373 ACAGTCGATCAATCCAGAAAGCGGCAATTTCCACCATGATATTCGGCAAGCAGGCATC 2314
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QY 4512 GCCATGGGTACGACGAGATCTCTCGCGTGGGCGATGCGCGCTTGAAGCTGCGCAACAG 4571
DB |||||
QY 2313 GCCATGGGTACGACGAGATCTCTCGCGTGGGCGATGCGCGCTTGAAGCTGCGCAACAG 2254
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QY 4572 TTGCGGTGGCGAGCGCCCTGATGCTCTTCTGTCAGATCATCTGATCGCAAGACCGGC 4631
DB |||||
QY 2253 TTGCGGTGGCGAGCGCCCTGATGCTCTTCTGTCAGATCATCTGATCGCAAGACCGGC 2194
DB |||||

RESULT 10

US-09-380-190A-18/c

; Sequence 18, Application US/09380190A

; Patent No. 6410220

; GENERAL INFORMATION:

; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.

; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES

; THEREOF

; NUMBER OF SEQUENCES: 74

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MUEITING, RAASCH & GERHARDT, P.A.

; STREET: 119 NORTH FOURTH STREET, SUITE 203

; CITY: MINNEAPOLIS

; STATE: MINNESOTA

; COUNTRY: USA

; ZIP: 55401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/380,190A

; FILING DATE: 26-Aug-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US98/03918

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RESULT 14
US-09-380-190A-15/c
; Sequence 15, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
; THEREOF
;
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,190A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/03918
FILING DATE: 28-FEB-98
ATTORNEY/AGENT INFORMATION:
NAME: MUEITING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 228.00010201
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 6359 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-380-190A-15
Query Match 27.1%; Score 1469.6; DB 3; Length 6359;
Best Local Similarity 92.0%; Pred. No. 7.5e-314; Indels 66; Gaps 2;
Matches 1600; Conservative 0; Mismatches 74;
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Job time : 877 secs

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